

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:04:19 ; Search time 1446 Seconds
(without alignments)
11509.559 Million cell updates/sec

Title: US-10-736-318-22
Perfect score: 2925
Sequence: 1 gttgttatttattggtgc.....tcaattggactaaatctg 2925

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 583141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sw.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	2835.2	96.9	103904 15 ATAC021640
2	1300.8	44.5	2294 15 AF105034
3	926.8	31.7	3004 15 AF069468
4	464.2	15.9	1163 15 AY088527
5	461	15.8	1175 6 ARS08874
6	461	15.8	1175 6 AX573146
7	461	15.8	1175 15 ATRNASC5D
8	428.2	14.6	1113 15 AK176721
9	347.2	11.9	846 6 AX505726
10	228.2	7.8	1104 15 AR231157
11	228	7.8	1155 15 AF081794
12	218.8	7.5	1148 15 AF099969
13	203.4	7.0	1447 6 AR237880
14	188	6.4	1210 15 BT009523
15	188	6.4	1210 15 BT009523
16	187	6.4	911 6 AR237878
17	184.8	6.3	1189 15 BT016653
18	179.6	6.1	1253 15 AK111908

19	179.6	6.1	1318	6	AR237879	AR237879 Sequence	
20	176.4	6.0	1242	15	AK112014	AK112014 Oryza sat	
21	173.8	5.9	1070	6	AR237871	AR237871 Sequence	
22	163.8	5.6	110000	15	AP008207_018	Continuation (19 o	
23	163.8	5.6	179428	15	AP003214	AP003214 Oryza sat	
24	161.8	5.5	1381	6	AX155063	AX155063 Sequence	
25	140.8	4.8	650	15	BT019106	BT019106 Zea mays	
26	138.8	4.7	446	6	BD273096	BD273096 Materials	
c	27	120.8	4.1	310	10	G71612	G71612 A65988234FM
28	118.4	4.0	300	6	AR249155	AR249155 Sequence	
c	29	118.2	4.0	293	10	G71681	G71681 A85715834FM
c	30	108.6	3.7	559	10	BV007175	BV007175 LS269 Mea
31	90.8	3.1	269	6	AR245020	AR245020 Sequence	
32	90	3.1	459	6	AR237873	AR237873 Sequence	
33	82.8	2.8	314	6	AR252099	AR252099 Sequence	
34	77.8	2.7	7218	6	I66494	I66494 Sequence 14	
35	74.6	2.6	110000	14	AP006485_1	Continuation (2 of	
36	72	2.5	282289	14	AC152242	AC152242 Bos tauru	
37	71.8	2.5	5693	14	AC084077	AC084077 Homo sapi	
c	38	71.6	2.4	13054	14	AC149986	AC149986 Strongylo
39	71	2.4	495	6	AR237874	AR237874 Sequence	
40	70.8	2.4	1328	15	AJ840631	AJ840631 Arabidops	
41	70.4	2.4	179206	8	CNS01DS6	AL121656 BAC sequ	
c	42	70.4	2.4	217543	14	AC163195	AC163195 Bos tauru
c	43	70.4	2.4	231912	14	AC087566	AC087566 Mus muscu
44	70	2.4	6668	6	AX346599	AX346599 Sequence	
45	70	2.4	340089	14	AC104922	AC104922 Mus muscu	

ALIGNMENTS

RESULT 1
ATAC021640 103904 bp DNA linear PLN 30-OCT-2002
LOCUS Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence,
DEFINITION complete sequence.
ACCESSION AC021640
VERSION AC021640.7 GI:12408747
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 103904)
AUTHORS Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.,
Wu,D., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence
Unpublished
2 (bases 1 to 103904)
AUTHORS Lin,X. and Kaul,S.
TITLE Direct Submission
JOURNAL Medical Center Dr., Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE 3 (bases 1 to 103904)
AUTHORS Lin,X.
TITLE Direct Submission
JOURNAL Medical Center Dr., Rockville, MD 20850, USA
COMMENT On Jan 24, 2001 this sequence version replaced gi:12280770.
Address all correspondence to:at@tigr.org

BAC clone F16B3 is from Arabidopsis chromosome III and is near the
molecular marker mi74.
The orientation of the sequence is from SP6 to T7 end of the BAC
clone.
Genes were identified by a combination of three methods: Gene
prediction programs including GRAIL (available by anonymous ftp
from arthur.epm.ornl.gov), Genefinder (Phil Green, University of
Washington), Genscan (Chris Burge,
http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene

(<http://www.cbs.dtu.dk/netgene/cbenetpgene.html>), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (<http://www.tigr.org/tdb/at/at.html>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES

source

1. 103904

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/map="mi74"
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/ecotype="Columbia"
<129. .>979

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/note="predicted by genefinder"
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mRNA

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CDS

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/translation="MEEKDWGSPILSENEAGLLCYDDBEYQFGGPAPKQLRYLSEIG
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AVNTYPSDEDESLCAAEFPQDRDSVTKLSDMHICDARVPVDVYLPNSQFKKSPGEP
SVYTCPSG"

gene

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/gene="F16B3.2"

/note="identical to COL2 GB:AAB67879 from [Arabidopsis

thaliana]"

mRNA

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SSMDQFQNVQTHQRFQSGGVVPLQVVEESTHLQSQNFQNGINYPGSSGAHYN
NNSLKDNLHSAVSSMDISVPPESTASDITVOHPRTKETIDQLSGPPTQVVOQLTPM
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repeat_region

5228. .5255

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gene

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mRNA

/note="predicted by genefinder"
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CDS

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NFGSDVVOAQSEHKLPPRRPRNNKRLAASDDPDPIESVQEKPKRTRGSSKQEENELP

gene

/note="predicted by genscan, contains Coesterase domain"
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10256. .>10518))

mRNA

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complement(<759. .>10518)

CDS

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/db_xref="GI:6957704"

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SGNSDGSPIRCQSPGRDIGHAAETYLIRLSFNLLGYLDLVIPTSDGLKP
VVVVTGGAIIIGYKANGSLGLQLABRDIIVACLDYRFPQGTISDMVSDAAQGISP
VNNISAPGDPNRIYLMQSGAGAHISCALEQNAIKESRGESISMSQIKAYRGLS
GGYNFLNLVHFHNRGLRYSIFLSIMEGESFKQSPVRRLKDLNVRKAALLPHIIL
FHGSADYSIPPEASCTFTDALQAAEVKAEVLVYKGTHTDLFLQDPLRGKDELFDHI
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gene

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13745. .13874,14237. .14456))

CDS

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SFMGTACSSLYSLYSGRPANMQGLVQFSIAAKDFIYICLTFVTSHLCLK
FALIPILCRALQVAKPLRRNFRSTIYRKYLEDPCVWVESNTTLNLSQAEIAG
FLIILSLWSQWNIOTFMVQLLKMVQAPVTAGYHQSTWBSRIGRTVTPIQRYAPP
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gene

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CDS

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SVKADGGTIYFGVTYFKGMVVDYDPDGLGLPDLAKYMRFPVDIHATLSVLVFGAV
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R"

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gene

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/note="predicted by genscan"

mRNA

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CDS

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Db	65393	TAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACATGAAATTTGAAATTTGTGT	65452
Qy	1979	TCCTAGTCTCATTTCTGCTGCTGCTCTCTATTTTGTGTTAGTATCATTCCTACGA	2038
Db	65453	TCCTAGTCTCATTTCTGCTGCTGCTCTCTATTTTGTGTTAGTATCATTCCTACGA	65512
Qy	2039	GAAAGGCAATGCTTTTGCRAATATACGTGGCAATGAAGGCTATGCCCTTGGTACACATCTTC	2098
Db	65513	GAAAGGCAATGCTTTTGCRAATATACGTGGCAATGAAGGCTATGCCCTTGGTACACATCTTC	65572
Qy	2099	TTCCAGTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAATGTTACTCTACACTTG	2158
Db	65573	TTCCAGTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAATGTTACTCTACACTTG	65632
Qy	2159	ACCAATTTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTATCTTGTGTTAGTTGAGT	2218
Db	65633	ACCAATTTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTATCTTGTGTTAGTTGAGT	65692
Qy	2219	TTATGATTTTATGGGTTTCAAAAGAGCTTCATGACATTAATTTCTCTATAAGCATCTCC	2278
Db	65693	TTATGATTTTATGGGTTTCAAAAGAGCTTCATGACATTAATTTCTCTATAAGCATCTCC	65752
Qy	2279	ATGCTACCCATCATATGTACAAAGCAAAACACACTCTCTCATTGGCGGTATGTCAA	2338
Db	65753	ATGCTACCCATCATATGTACAAAGCAAAACACACTCTCTCATTGGCGGTATGTCAA	65812
Qy	2339	AGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGCTGATCTTTTACTTTGAT	2398
Db	65813	AGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGCTGATCTTTTACTTTGAT	65872
Qy	2399	GTTTTTCCGGTTCCTCAGGCTCGCATTCATCCATCCGCTGGAGGATATCTCAGGCTATACC	2458
Db	65873	GTTTTTCCGGTTCCTCAGGCTCGCATTCATCCATCCGCTGGAGGATATCTCAGGCTATACC	65932
Qy	2459	GCACGTGATAGCGCTGTTATAGTGGGATTCATCTCATCAACACATCTGAGCTTTTGT	2518
Db	65933	GCACGTGATAGCGCTGTTATAGTGGGATTCATCTCATCAACACATCTGAGCTTTTGT	65992
Qy	2519	TTTGGGAAGGATATGACACAGCATCCATGATTCATCATGATGATGATGATGATGATGAT	2578
Db	65993	TTTGGGAAGGATATGACACAGCATCCATGATTCATCATGATGATGATGATGATGATGAT	66052
Qy	2579	AATGGGTGCAAGGATACCATACCAACCAACATACCAACATACCAACATACCAACATACCA	2638
Db	66053	AATGGGTGCAAGGATACCATACCAACCAACATACCAACATACCAACATACCAACATACCA	66112
Qy	2639	TACCATATGATGGAGTGGATGTTTGGCTCTCTATGTTCTTATGTTCTTATGAGCAAAAGACAG	2698
Db	66113	TACCATATGATGGAGTGGATGTTTGGCTCTCTATGTTCTTATGTTCTTATGAGCAAAAGACAG	66172
Qy	2699	TTTCAAGGAGAAAGAAAGTGAATGTTTCAATGCTCACAATGATGATGATGATGATGATGAT	2758
Db	66173	TTTCAAGGAGAAAGAAAGTGAATGTTTCAATGCTCACAATGATGATGATGATGATGATGAT	66232
Qy	2759	CTTCTCGTACTCTTATTAACACCTTTCTAATCACTTTGGTGGAAATTAACACATGACTG	2818
Db	66233	CTTCTCGTACTCTTATTAACACCTTTCTAATCACTTTGGTGGAAATTAACACATGACTG	66292
Qy	2819	CATAATTTGATGCAAGTTTTCAGACTTTTATGCTTAAATCTCTGATGATGATGATGATGATGAT	2878
Db	66293	CATAATTTGATGCAAGTTTTCAGACTTTTATGCTTAAATCTCTGATGATGATGATGATGATGAT	66352
Qy	2879	CAATTTATATATTTGCTGGATGAAGAG-TTCAAAATTTGGACTTAAATCTG 2925	
Db	66353	CAATTTATATATTTGCTGGATGAAGAGTTTCAAAATTTGGACTTAAATCTG 66400	

RESULT 2
AF105034

LOCUS	AF105034	2294 bp	DNA	linear	PLN 10-JUN-1999
DEFINITION	Arabidopsis thaliana delta7 sterol C-5 desaturase (STE1) gene, complete cds.				
ACCESSION	AF105034				
VERSION	AF105034.1	GI:5031218			
KEYWORDS	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
AUTHORS	Choe, S., Neguchi, T., Fujioka, S., Takatsuto, S., Tissier, C. P., Gregory, B. D., Ross, A. S., Tanaka, A., Yoshida, S., Tax, F. E. and Feldmann, K. A.				
TITLE	The Arabidopsis dwf7/ste1 mutant is defective in the delta7 sterol C-5 desaturation step leading to brassinosteroid biosynthesis				
JOURNAL	Plant Cell 11 (2), 207-221 (1999)				
PUBMED	9927639				
AUTHORS	Choe, S., Tanaka, A., Gregory, B. D. and Feldmann, K. A.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-NOV-1998) Plant Sciences, The University of Arizona, Forbes Hall 303, Tucson, AZ 85721, USA				
FEATURES	Location/Qualifiers				
Source	1..2294				
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	/chromosome="III"				
	/map="2.2"				
	/ecotype="Ws-2"				
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CDS	/product="delta7 sterol C-5 desaturase"				
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variation	1552				
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	/replace="a"				
ORIGIN					
Query Match	44.5%; Score 1300.8; DB 15; Length 2294;				
Best Local Similarity	98.8%; Pred. No. 1e-233;				
Matches 1352; Conservative	0; Mismatches 12; Indels 4; Gaps 4;				
Qy	1	GTTTGGTATTTATGGATGCACAGAGCGCTTCATGACATTAGCCCTCTCTATAGTATCT	60		
Db	929	GTTTGGTATTTATGGATGCACAGAGCGCTTCATGACATTAGCCCTCTCTATAGTATCT	988		
Qy	61	CCATGCCACCCATCATATCTACAAAGCAGATACACTCTCTCCATTTGCCGCTAAGTG	120		
Db	989	CCATGCCACCCATCATATCTACAAAGCAGATACACTCTCTCTCCATTTGCCGCTAAGTG	1048		

QY 121 TTTTCAGTTGTTCTTCTTTAGTTCTTTGTAAGAATGTTGTTAGTATTTAGTTCTTACCAG 180
Db TTTTCAGTTGTTCTTCTTTAGTTCTTTGTAAGAATGTTGTTAGTATTTAGTTCTTACCAG 1108
QY 181 AAAAGACTTTGTCAGCAGCTGCTGTGACTCCAAATCACATTTGCAATTCCTTATCCATAA 240
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QY 241 AGTAACAGAAAGGCTAGAAATATATATAAATGTGAGCTGCAATTTACATATGTCCAGAG 300
Db AGTAACAGAAAGGCTAGAAATATATATAAATGTGAGCTGCAATTTACATATGTCCAGAG 1228
QY 301 AGACTTCTGACTTAACAGAGTTTAGATCTTTGTGTTTCTTCTGCTTCGGACTGATTT 360
Db AGACTTCTGACTTAACAGAGTTTAGATCTTTGTGTTTCTTCTGCTTCGGACTGATTT 1288
QY 361 GGAATATGACGAGAGTTCTTTATCTACTTCCCTGGAGTGTATCTTGGTTTAATCCAAAG 420
Db GGAATATGACGAGAGTTCTTTATCTACTTCCCTGGAGTGTATCTTGGTTTAATCCAAAG 1348
QY 421 TGTGACATCTAAATATTACTTGTAACTTCTTACGTTTTTGTTCACAGGCTTGCA-TTC 479
Db TGTGACATCT-AAATATTACTTGTAACTTCTTACGTTTTTGTTCACAGGCTTGCA-TTC 1407
QY 480 ACCAGTAGACGGGATCTTAAGGCTGTACCGCATGTGATAGCGCTG-TTATAGTGCCAA 538
Db ACCAGTAGACGGGATCTTACGGCTGTACCGCATGTGATAGCGCTGTTTATAGTGCCAA 1467
QY 539 TTTCAATTCACACTCATATAGTCTTTTGTTCATGGAAGGATATGAGCGGCATATCC 598
Db TTTCAATTCACACTCATATAGTCTTTTGTTCATGGAAGGATATGAGCGGCATATCC 1527
QY 1468 TTTCAATTCACACTCATATAGTCTTTTGTTCATGGAAGGATATGAGCGGCATATCC 658
Db TTTCAATTCACACTCATATAGTCTTTTGTTCATGGAAGGATATGAGCGGCATATCC 1587
QY 599 ATGACTGTGATCCATGCAACATCTGCGCAGTAATGGTGCAGGATACCATAGATACACC 658
Db ATGACTGTGATCCATGCAACATCTGCGCAGTAATGGTGCAGGATACCATAGATACACC 1587
QY 659 ACACGATACCAAGCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 718
Db ACACGATACCAAGCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1647
QY 719 CTTCTAGGATCTCTCTTAGAGAGATGACAAACAGACAGCTTCAAGAACGAGT 778
Db CTTCTAGGATCTCTCTTAGAGAGATGACAAACAGACAGCTTCAAGAACGAGT 1707
QY 779 GAGAATGCCACTTGGTTTGTCTTCTGTTTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 838
Db GAGAATGCCACTTGGTTTGTCTTCTGTTTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1767
QY 839 TCAGCCTTTCTGTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 898
Db TCAGCCTTTCTGTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1827
QY 899 ATTATATGTTTCAAAATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 958
Db ATTATATGTTTCAAAATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1887
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Db 2247 TTTAAATAAATCATCGTAACCTCCACTTCAAAAATCTTTTAAAAA 2294
RESULT 3
AF069468
LOCUS 3004 bp DNA linear PLN 19-MAY-1999
DEFINITION Arabidopsis thaliana sterol-C5-desaturase gene, complete cds.
ACCESSION AF069468
VERSION AF069468.1 GI:4234767
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
REFERENCE 1 (bases 1 to 3004)
Huselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.
Delta7-sterol-C5-desaturase: molecular characterization and
functional expression of wild-type and mutant alleles
Plant Mol. Biol. 39 (5), 891-906 (1999)
10344195
PUBMED
REFERENCE 2 (bases 1 to 3004)
Huselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.
Direct Submission
TITLE
Submitted (30-MAY-1998) IBMP, 28, rue Goethe, Strasbourg 67083,
France
FEATURES
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FKAB"
CDS
Query Match 31.7%; Score 926.8; DB 15; Length 3004;
Best Local Similarity 99.5%; Pred. No. 1.2e-163;
Matches 961; Conservative 0; Mismatches 2; Indels 3; Gaps 3;
QY 1 GTTTGGTATTATTGGATGTCACAGAGCTTCATGACATTAAGCCTCTCTATAAGTATCT 60
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QY 61 CCATCCCAACCATATCTCAACAAGCAGAAATACCTCTCTCCATTTGCCGGTAAGTG 120
Db 2089 CCATCCCAACCATATCTCAACAAGCAGAAATACCTCTCTCCATTTGCCGGTAAGTG 2148
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Db 2149 TTTTCAGTTTGTCTTTTCTTTTGTAGTTCTTTGTAAGAATGTTGTTAGTATTTAGTTCTTACCAG 2208
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Db 1151 TAAATGTTTGATG 1163

RESULT 5
AR608874
LOCUS AR608874 1175 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 23 from patent US 6822142.
ACCESSION AR608874
VERSION AR608874.1 GI:56663610
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1175)
AUTHORS Karunanandaa,B., Post-Beittenmiller,M., Venkatramesh,M.,
Kishore,G.M., Thorne,G.M. and LeDeaux,J.R.
TITLE Transgenic plants containing altered levels of steroid compounds
JOURNAL Patent: US 6822142-A 23 23-NOV-2004;
Monsanto Company; St. Louis, MO
FEATURES
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1. .1175
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Best Local Similarity 97.6%; Pred. No. 3.3e-76;
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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Db 643 TTTGCCGGGCTTGCAATTTCCACCAGTAGCGGATCTTTCAGGCTGTACCGCATGTGATA 702
Qy 521 GCGCTG-TTATAGTGCCAAATTCATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCG 579
Db 703 GCGCTGTTTATAGTGCCAAATTCATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCG 762
Qy 580 ATATGGAACGGCGAACAATCCATGATCGATCCATGGCAACATCTGGCCAGTAATGGGTGCA 639
Db 763 ATATGGCGGGCGAACAATCCATGATCGATCCATGGCAACATCTGGCCAGTAATGGGTGCA 822
Qy 640 GGATACCATACGATACACACAGCATACAGCATAACTATGGTCAATATACCATATGG 699
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Qy 700 ATGGATTTGGATGTTTGGCTCTCTTAGGGATCCCTCTTAGAAGAAGATGACAAACAGAC 759
Db 883 ATGGATTTGGATGTTTGGCTCTCTTAGGGATCCCTCTTAGAAGAAGATGACAAACAGAC 942
Qy 760 AGCTTCAAGAAAGCAGAGTGAGAAATGCCCACTTTGGGTTTGTCTCTGTTTGTCTTGT 819
Db 943 AGCTTCAAGAAAGCAGAGTGAGAAATGCCCACTTTGGGTTTGTCTCTGTTTGTCTTGT 1002
Qy 820 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTGTTCTTTTCTTTCTTTCTTTATTCATGT 879
Db 1003 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTGTTCTTTTCTTTCTTTCTTTATTCATGT 1062
Qy 880 GTCTCTCTCAACCTTTCCAAATATATGTTTACAAACATTTGCTGTCTAGTTTAAACATG 939
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RESULT 7
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Qy 940 TAAATGTTTGATGATCTTTTC 960
Db 1123 TAAATGTTTGATGATCTTTTC 1143

RESULT 6
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LOCUS AX573146 1175 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 23 from Patent WO2061072.
ACCESSION AX573146
VERSION AX573146.1 GI:26005070
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Karunanandaa,B., Post-Beittenmiller,M., Venkatramesh,M.,
Kishore,G.M., Thorne,G.M. and LeDeaux,J.
TITLE Transgenic plants containing altered levels of steroid compounds
JOURNAL Patent: WO 02061072-A 23 08-AUG-2002;
Monsanto Technology LLC (US)
FEATURES
source
1. .1175
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ORIGIN
Query Match 15.8%; Score 461; DB 6; Length 1175;
Best Local Similarity 97.6%; Pred. No. 3.3e-76;
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

Qy 462 TTTACAGGGCTTGCA-TTCAACCAGTAGCGGATCTTAAGCTGTACCGCATGTGATA 520
Db 643 TTTGCCGGGCTTGCAATTTCCACCAGTAGCGGATCTTTCAGGCTGTACCGCATGTGATA 702
Qy 521 GCGCTG-TTATAGTGCCAAATTCATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCG 579
Db 703 GCGCTGTTTATAGTGCCAAATTCATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCG 762
Qy 580 ATATGGAACGGCGAACAATCCATGATCGATCCATGGCAACATCTGGCCAGTAATGGGTGCA 639
Db 763 ATATGGCGGGCGAACAATCCATGATCGATCCATGGCAACATCTGGCCAGTAATGGGTGCA 822
Qy 640 GGATACCATACGATACACACAGCATACAGCATAACTATGGTCAATATACCATATGG 699
Db 823 GGATACCATACGATACACACAGCATACAGCATAACTATGGTCAATATACCATATGG 882
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Db 1123 TAAATGTTTGATGATCTTTTC 1143

RESULT 7
ATRNASC5D
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(E-mail: brassin@affrc.go.jp, Tel: 81-29-838-8392,
Fax: 81-29-838-8392)

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Best Local Similarity 60.9%; Pred. No. 1.5e-32;			
Matches 443; Conservative 0; Mismatches 198; Indels 86; Gaps 1;			
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Dd	405	TGTTGAGTTGGGCATCTATTTGGATG CACAGAGAGTTGCATGATATCA AACCCTCTTTACAA	464
Qy	2271	GCA TCCTCAGTCTACCATCATATG TATACA CAAGCAAAA CACATCTCTCCATTTGCCGG	2330
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Qy	2331	TATGTC AAAAGCTATATGTTCTCA ATCTAAATTC AAGAGCTTGTATCAATGGTGACTTCTTT	2390
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Dd	521	-----CTGGGTTGGCGTTCCACGCTATAGACGGGATAC TCAG	558
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Dd	559	CGGATCCAC ANATGNTATCGCGCTGTTTCTTGTG CCAACATTTTCATGACACACATTTCTG	618
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Qy	2691	AAAGACA	2697
Db	799	GAGGCCA	805
RESULT 11			
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LOCUS			
DEFINITION	Nicotiana tabacum sterol-C5(6)-desaturase mRNA, complete cds.		
ACCESSION	AF081794		
VERSION	AF081794.1	GI:4140397	
KEYWORDS			
SOURCE	Nicotiana tabacum (common tobacco)		
ORGANISM	Nicotiana tabacum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana.		
AUTHORS	1 (bases 1 to 1155)		
TITLE	Husselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.		
JOURNAL	Delta7-sterol-C5-desaturase; molecular characterization and functional expression of wild-type and mutant alleles		
PUBMED	Plant Mol. Biol. 39 (5), 891-906 (1999)		
REFERENCE	10344195		
AUTHORS	2 (bases 1 to 1155)		
TITLE	Benveniste,P.		
JOURNAL	Direct Submission		
FEATURES	Submitted (30-JUL-1998) Plant Molecular Biology Institute, Centre National de la Recherche Scientifique, 28 rue Goethe, Strasbourg 67084, France		
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Best Local Similarity	61.1%	Pred. No. 1.6e-32;	
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Qy	2033	CTACGAGAAGCGAATGCTTTTGGCAATATACGTGGCAATGAAGGCTATGCCCTTGGTACA	2092
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Qy	2093	CTCTTCTTCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAATGTTACTCTA	2152
Db	389	GTGCCCTTCATCACTTCTTGAGTACATGATCGAAATGAGATGCAATAATGTTTGC	448
Qy	2153	CACCTTGACCAATTTCAACTGGTTCTCTGTTTCCTCTACATAGCTCTCTATCTTGT	2212
Db	449	GAATAAGTGATGTGGATGCTTTCCTATGTTATCTATCGGCTATTTATCTTGT	508
Qy	2213	TTGAGTTTATGATTTATTTGCGGTTACAAAGAGCTTCATGACATTAATTTCTCTAT	2272
Db	509	TGGAGTTTGGGATCTACTCTGGATGCATATGAGTTGCAATGACATAAACCTCTGT	568

TITLE Sterol metabolism enzymes
JOURNAL Patent: US 6465717-A 27 15-OCT-2002;
E. I. du Pont de Nemours and Company; Wilmington, DE;
EPX;

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 7.0%; Score 203.4; DB 6; Length 1447;
Best Local Similarity 61.3%; Pred. No. 6.1e-28;
Matches 399; Conservative 0; Mismatches 166; Indels 86; Gaps 1;
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DB 376 GCCTTGGTACTCTTTACTTCCAACTGTTCGGAGTACCTGGTAGAAACTGGCTGGACAA 435
QY 2142 ANGTTACTCTACACTTGAACATTCAACTGGTTCCTCTGTTCCTCTACATAGCTCTCTA 2201
DB 436 GTGCTATCTCTAGATTATATAATGTGGTTGGCTTGCAATACCTTGTGTATTTAGCAATTTA 495
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QY 2262 TCTCTATAAGCATCTCCATGCTACCATCATATGTACAACAGCAAAACACACTCTCTCC 2321
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DB 629 -----GCAFTTCACCCCTCTTGATGG 649
QY 2442 ATACTTCAGGCTATACCGACGTGATAGCGCTGTTTATAGTGCCGATTCATCTCATAAACA 2501
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QY 2502 CATCTGAGTCTTTTGTGTTTGGAGGATATGACAGCAAGCATCCATGATGATGATCAT 2561
DB 710 CATTTGGCCCTCATATTCATTTGAGGGCGTTTGGACTGCAAAATTCATGATTCATTCAT 769
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DB 770 GGAATAATGTTGGCTGTATGAGTGGTGTGTTTACCAACCATTCATCACACTCATATCGG 829
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DB 830 CACAACCTAGGCCCACTACACCATATGGATGGATGGATGTTTGGAACTCTT 880

RESULT 14
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LOCUS AR237881 1210 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 29 from patent US 6465717.
ACCESSION AR237881
VERSION AR237881.1 GI:27282714
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1210)
Famodu, O. O. and Rafaleki, J. A.
TITLE Sterol metabolism enzymes
JOURNAL Patent: US 6465717-A 29 15-OCT-2002;

E. I. du Pont de Nemours and Company; Wilmington, DE;
EPX;
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source Location/Qualifiers
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ORIGIN

Query Match 6.4%; Score 188; DB 6; Length 1210;
Best Local Similarity 59.8%; Pred. No. 4.9e-25;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;
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QY 2202 TCTGTTTTAGTTGAGTTTATGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAATTT 2261
DB 368 TCTCATCTTTGGAGTTCCGGAATTTACTGGATGCACAGAGATTGTCATGACATAAGCC 427
QY 2262 TCTCTATAAGCATCTCCATGCTACCATCATATGTACAACAGCAAAACACACTCTCTCC 2321
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QY 2322 ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
DB 488 ATTTG----- 492
QY 2382 TGACTTCTTTACTTGATGTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGG 2441
DB 493 -----CTGGACTAGCATTCATCCATTTGGACGG 521
QY 2442 ATACTTCAGGCTATACCGACGTGATAGCGCTGTTTATAGTGCCGATTCATCTCATAAACA 2501
DB 522 ATACTGCAAGCCATATCGCACGTGATGCTGTCTTCTCTCCGATGCACTTCAGGACG 581
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DB 642 GCGAAGATCTGCGCGTGTATGGCGCGGCTACCAACCATCCACACAGCATACCGG 701
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RESULT 15
BT009523
LOCUS BT009523 1210 bp mRNA linear PLN 20-JUN-2003
DEFINITION Triticum aestivum clone wr1.pk0107.a5:file, full insert mRNA
sequence.
ACCESSION BT009523
VERSION BT009523.1 GI:32129074
KEYWORDS FLI_CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE
1 (bases 1 to 1210)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
Tingey, S. V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H.,
Caraher, N. R., Hanafey, M. K. and Hainey, C. F.

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		Match	%				
1	2925	100.0	2925	6	ABK89916		Abk89916 Gene enco
2	2925	100.0	2925	12	ADQ28843		Adq28843 Arabidops
3	924.4	31.6	1889	6	ABK89915		Abk89915 Gene enco
4	924.4	31.6	1889	12	ADQ28841		Adq28841 Thale cre
5	464.2	15.9	1164	3	AAC41897		Aac41897 Arabidops
6	461	15.8	1175	6	ABS53044		Abs53044 Arabidops
7	347.2	11.9	846	6	ABZ12616		Abz12616 Arabidops
8	203.4	7.0	1447	8	ABX15834		Abx15834 cDNA enco
9	203.4	7.0	1447	12	ADI19006		Adi19006 Soybean s
10	189.4	6.5	833	12	ADI45356		Adi45356 Rice isop
11	188	6.4	1135	12	ADI45599		Adi45599 Wheat iso
12	188	6.4	1210	8	ABX15835		Abx15835 cDNA enco
13	188	6.4	1210	12	ADI19008		Adi19008 Wheat ste
14	187	6.4	911	8	ABX15832		Abx15832 cDNA enco
15	187	6.4	911	12	ADI19002		Adi19002 Maize ste
16	184.4	6.3	828	12	ADI45677		Adi45677 Corn isop
17	179.6	6.1	825	12	ADK14887		Adk14887 Rice OBDW
18	179.6	6.1	1318	8	ABX15833		Abx15833 cDNA enco
19	179.6	6.1	1318	12	ADI19004		Adi19004 Rice ster

XX	(CHOE/) CHOE S.
PA	(FELD/) FELDMANN K A.
XX	
PI	Choe S, Feldmann KA;
XX	
DR	WPI; 2002-582494/62.
DR	P-PSDB; AAU99580.
XX	
PT	Novel isolated dwarf polynucleotide for altering sterol composition of a
PT	plant, by introducing polynucleotide into plant cell to produce
PT	transformed plant cell and producing transgenic plant from transformed
PT	cell.
XX	
PS	Claim 7; Fig 10; 53pp; English.
XX	
CC	The present invention relates to the isolation of dwarf7 (dwf7) mutants
CC	and encoding polynucleotides that impart at least one dwf7 mutant
CC	phenotype when expressed in a plant. The polynucleotide sequences
CC	encoding the mutant dwf7 proteins are useful for producing transgenic
CC	plants from transformed plant cells. The polynucleotide sequences are
CC	useful for altering the sterol composition of a plant relative to the
CC	wild-type plant. The transgenic plant has less cholesterol or increased
CC	sterol production relative to the wild-type plant. The mutant sequences
CC	are also useful for isolating or creating other mutant cell gene alleles,
CC	and for detecting plant regulatory defects which can affect plant growth.
CC	The present sequence encodes Arabidopsis thaliana dwf7 homologue protein,
CC	HDP7
XX	
SQ	Sequence 2925 BP; 779 A; 603 C; 510 G; 1033 T; 0 U; 0 Other;
Query Match 100.0%; Score 2925; DB 6; Length 2925;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 2925; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GTTTGGTATTTATTGGATGCAAGAGCGCTTCATGACATAAAGCCTCTCTATAAGTATCT 60
Db	1 GTTTGGTATTTATTGGATGCAAGAGCGCTTCATGACATAAAGCCTCTCTATAAGTATCT 60
Qy	61 CCATGCCACCACCATCATATCTACTACAACAGCAGAAACACTCTCCATTTGCCGTGAAGTG 120
Db	61 CCATGCCACCACCATCATATCTACTACAACAGCAGAAACACTCTCTCCATTTGCCGTGAAGTG 120
Qy	121 TTTTCAGTTCTCTCTTTTAGTTCTCTGTAAAAGATTGGTAGCATTTAGTTTCTTTACCAAG 180
Db	121 TTTTCAGTTCTCTCTTTTAGTTCTCTGTAAAAGATTGGTAGCATTTAGTTTCTTTACCAAG 180
Qy	181 AAAAGACTTTGTGCAGAGCTGCTTGTAATCCAATCACATTTTGCATTCCTTATCCATAAA 240
Db	181 AAAAGACTTTGTGCAGAGCTGCTTGTAATCCAATCACATTTTGCATTCCTTATCCATAAA 240
Qy	241 AGTAACCGAAAGGCTAGAAATATATAATGTCCAGCTGCATTACTTTCACATATGTCAGAG 300
Db	241 AGTAACCGAAAGGCTAGAAATATATAATGTCCAGCTGCATTACTTTCACATATGTCAGAG 300
Qy	301 AGACTCTCGACTTAACCGAGGTTAGATCTTTTGTGTTCTCTCTCGGTCTCGGACTGATT 360
Db	301 AGACTCTCGACTTAACCGAGGTTAGATCTTTTGTGTTCTCTCTCGGTCTCGGACTGATT 360
Qy	361 GGAAATGACGAGAAGTCTTTTATATCTACTTCCCTGGAGTGATCTTGTGTTAATCCAAGGA 420
Db	361 GGAAATGACGAGAAGTCTTTTATATCTACTTCCCTGGAGTGATCTTGTGTTAATCCAAGGA 420
Qy	421 TGTCACATCTAAAAATATTAATCTTGTAACCTTCCCTTAAGTTTTGTTACAGGGCTTGATCA 480
Db	421 TGTCACATCTAAAAATATTAATCTTGTAACCTTCCCTTAAGTTTTGTTACAGGGCTTGATCA 480
Qy	481 CCCAGTAGACGGGATACCTTAAGGCTGTATCCGCACTGTATAGCGCTGTATAGTGCCAATT 540
Db	481 CCCAGTAGACGGGATACCTTAAGGCTGTATCCGCACTGTATAGCGCTGTATAGTGCCAATT 540
Qy	541 CATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCGATATGGAAGCGCAACATCCAT 600

1681 TCTCTGGTCTCTACATCTATTACCTTAAACTCAACGTTTACGTCGCCAAAGGTTACT 1740
1681 TCTCTGGTCTCTACATCTATTACCTTAAACTCAACGTTTACGTCGCCAAAGGTTACT 1740
1741 TTTTTCAAATTCGATGCTCTGTTTGAACCTTTCTTTTGGTGGATTCCTTCGATGATC 1800
1741 TTTTTCAAATTCGATGCTCTGTTTGAACCTTTCTTTTGGTGGATTCCTTCGATGATC 1800
1801 GCGTAGATAGTGTGTATACGTTAACTTTTCTTACTGTGTTACTTTTCAGTCTCTGTC 1860
1801 GCGTAGATAGTGTGTATACGTTAACTTTTCTTACTGTGTTACTTTTCAGTCTCTGTC 1860
1861 TTCTACTCTCTCAATTAATAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAA 1920
1861 TTCTACTCTCTCAATTAATAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAA 1920
1921 AGTTGAATCTTCATGAAATTTGAGCTCAAAATATATACCATGAAATTTGAAATTTGTTGTT 1980
1921 AGTTGAATCTTCATGAAATTTGAGCTCAAAATATATACCATGAAATTTGAAATTTGTTGTT 1980
1981 TTAGTTCTATTTCTGCTTGGTTTCTTCTATTTTGTGGTTAGAAATCCATTCCTACGAGA 2040
1981 TTAGTTCTATTTCTGCTTGGTTTCTTCTATTTTGTGGTTAGAAATCCATTCCTACGAGA 2040
2041 AAGGCAATGCTTTTGCAAAATATACGTTGCAATGAAGGCTATGCTTTGGTACACTCTCTT 2100
2041 AAGGCAATGCTTTTGCAAAATATACGTTGCAATGAAGGCTATGCTTTGGTACACTCTCTT 2100
2101 CCAGCTGTCTGAGTATATGATCGAGCATGTTGGACCAATGTTTACTCTACACTTGAC 2160
2101 CCAGCTGTCTGAGTATATGATCGAGCATGTTGGACCAATGTTTACTCTACACTTGAC 2160
2161 CATTTCAACTGTTCTCTGTTTCTCTACATAGCTCTCTATCTGTTTGTAGTTGAGTTT 2220
2161 CATTTCAACTGTTCTCTGTTTCTCTACATAGCTCTCTATCTGTTTGTAGTTGAGTTT 2220
2221 ATGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAATTTCTCTATAAGCATCTCCAT 2280
2221 ATGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAATTTCTCTATAAGCATCTCCAT 2280
2281 GCTACCCATCATATGATGACCAAGCAACACACTCTCTCCATTTGCGGTATGTCGAAG 2340
2281 GCTACCCATCATATGATGACCAAGCAACACACTCTCTCCATTTGCGGTATGTCGAAG 2340
2341 CTATATGTTCTCAATCTAAATCAAGAGCTTGTATCAATGGTGAATCTTTTACTTGTATG 2400
2341 CTATATGTTCTCAATCTAAATCAAGAGCTTGTATCAATGGTGAATCTTTTACTTGTATG 2400
2401 TTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGGATCTTCAGGCTATACCGC 2460
2401 TTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGGATCTTCAGGCTATACCGC 2460
2461 AGTGTATAGCGCTGTTTATGTCGCAATTCATCTCATACATCTGAGTCTTTGTTTTT 2520
2461 AGTGTATAGCGCTGTTTATGTCGCAATTCATCTCATACATCTGAGTCTTTGTTTTT 2520
2521 TGGAGGGATATGGACAGCAAGCATCCATGATTGTCATACATGTTGAATCATGTTGACCTATAA 2580
2521 TGGAGGGATATGGACAGCAAGCATCCATGATTGTCATACATGTTGAATCATGTTGACCTATAA 2580
2581 TGGGTCAGGATACCATACCATACACATACATACATACATACATACATACATACATACAT 2640
2581 TGGGTCAGGATACCATACCATACACATACATACATACATACATACATACATACATACAT 2640
2641 CCATATGATGAGTGGATGTTGGTCTCTTATGTTTCTTTAGCAGAAAAGACAGTT 2700
2641 CCATATGATGAGTGGATGTTGGTCTCTTATGTTTCTTTAGCAGAAAAGACAGTT 2700
2701 TCAAGGAGAGAGAAAGTGCAGATGTTCAATGCTACATGTTCTTCTATATGTTGCTCT 2760
2701 TCAAGGAGAGAGAAAGTGCAGATGTTCAATGCTACATGTTCTTCTATATGTTGCTCT 2760

2761 TCTCTGACTCTTATTAACCTTTCTTAATCACTTTGGTGGATTAACCAATGACTGCA 2820
2761 TCTCTGACTCTTATTAACCTTTCTTAATCACTTTGGTGGATTAACCAATGACTGCA 2820
2821 TAAATTTGATGCAAGTTTCAGACTTTTATTTGCTTAAATCTCTGATGATTATTAACCTCA 2880
2821 TAAATTTGATGCAAGTTTCAGACTTTTATTTGCTTAAATCTCTGATGATTATTAACCTCA 2880
2881 ATTATATAATTTGCTGATGAGAGTTCAAAATTTGGACTAAATCTG 2925
2881 ATTATATAATTTGCTGATGAGAGTTCAAAATTTGGACTAAATCTG 2925

RESULT 2
ADQ28843

ID ADQ28843 standard; DNA; 2925 BP.

XX AC ADQ28843;

XX DT 23-SEP-2004 (first entry)

XX Arabidopsis DWF7/STEL homologue DNA.

XX STE1; dwarf7; dwf7; sterol; plant breeding; agricultural production;
KW flowering; leaf production; fruit production; branching; seed production;
KW cholesterol; brassinosteroid; sterol synthesis; DWF7/STEL; gene; ds.

XX Arabidopsis.

XX US2004133948-A1.

XX PD 08-JUL-2004.

XX PF 15-DEC-2003; 2003US-00736318.

XX PR 02-FEB-2000; 2000US-0179901P.

XX PR 02-FEB-2001; 2001US-00775879.

XX (ARIZ-) ARIZONA BOARD OF REAGENTS.

XX PI Choe S, Feldmann KA;

XX WPI; 2004-517063/49.

XX DR P-PSDB; ADQ28844.

XX DR GENBANK; AAF32466.

XX New isolated dwarf 7 (dwf7) polynucleotide, useful for conferring desired
PT traits on essentially any plant and for altering sterol composition of a
PT plant thus increasing or reducing cholesterol content.

XX Claim 6; SEQ ID NO 22; 52pp; English.

XX The invention relates to an isolated dwarf7 (dwf7) polynucleotide that
CC imparts at least one dwf7 mutant phenotype when expressed in a plant. The
CC invention also relates to a recombinant vector comprising the dwf7
CC polynucleotide and control elements that are operably linked to the
CC polynucleotide where a coding sequence within the polynucleotide can be
CC transcribed and translated in a host cell, and at least one of the
CC control elements is heterologous to the coding sequence, a host cell
CC transformed with the recombinant vector above, a method of producing a
CC DWF7 polypeptide, a transgenic plant comprising the polynucleotide, a
CC method of producing a transgenic plant and a method of altering the
CC sterol composition of a plant relative to the wild-type plant. The dwf7
CC polynucleotides and polypeptides are useful for producing transgenic
CC plants which display at least one dwf7 phenotype, so that the resulting
CC plants have altered structure or morphology. The transgenic plants are
CC useful in plant breeding, in agricultural production or in industrial
CC applications. The dwf7 polynucleotides are useful for isolating or
CC creating other mutant alleles and for enhancing certain features such as
CC flowering, producing larger leaves or fruit, increased branching and
CC increased seed production. They are also useful for conferring desired
CC traits on any plant, for altering sterol composition of a plant thus
CC increasing or reducing cholesterol content and for providing a tool for

CC studying the biosynthesis of brassinosteroids. The dwf7 control element
CC is useful as a plant promoter to express any protein of interest in a
CC transgenic plant, particularly to express a protein involved in
CC brassinosteroid biosynthesis. The Dwf7 polypeptide is involved in any
CC biochemical applications, e.g., regulation of sterol synthesis,
CC modification of elongation of plant structures and experimental or
CC industrial biochemical applications. This sequence represents DNA
CC encoding an Arabidopsis DWf7/STB1 polypeptide homologue, used in the
CC scope of the invention.

XX
SQ Sequence 2925 BP; 779 A; 603 C; 510 G; 1033 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2925;	DB 12;	Length 2925;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2925;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GTTTGGTATTATTTGGATGACAGAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT	60
DB	1	GTTTGGTATTATTTGGATGACAGAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT	60
QY	61	CGATGCCACCCATCATCTACAAACAGCAGATACACTCTCTCCATTTGCCGGTAAGTG	120
DB	61	CCATGCCACCCATCATCTACAAACAGCAGATACACTCTCTCCATTTGCCGGTAAGTG	120
QY	121	TTTTTCAGTTTGTCTTCTTTAGTTCTTTGTAAGATTTGGTAGCATTTAGTTTCTTACACAG	180
DB	121	TTTTTCAGTTTGTCTTCTTTAGTTCTTTGTAAGATTTGGTAGCATTTAGTTTCTTACACAG	180
QY	181	AAAAGACTTTGTGACAGCTGCTTTGACTCCAAATCACATTTTGTGCATTCCTTATCCATAA	240
DB	181	AAAAGACTTTGTGACAGCTGCTTTGACTCCAAATCACATTTTGTGCATTCCTTATCCATAA	240
QY	241	AGTAAACAGAAAGGCTAGAAATTAATAAATGTCAGCTGCATTAATTTACATATGTCAGAG	300
DB	241	AGTAAACAGAAAGGCTAGAAATTAATAAATGTCAGCTGCATTAATTTACATATGTCAGAG	300
QY	301	AGACTTCTGACTTAAACAGAGTTTGTAGATCTTTGTGTTTCTCTCTGCTCTCGGACTGAT	360
DB	301	AGACTTCTGACTTAAACAGAGTTTGTAGATCTTTGTGTTTCTCTCTGCTCTCGGACTGAT	360
QY	361	GGAAATGACAGAGAGTTCTTTTATCTACTTCCCTGGAGTGATCTTTGGTTAATCCAAAGG	420
DB	361	GGAAATGACAGAGAGTTCTTTTATCTACTTCCCTGGAGTGATCTTTGGTTAATCCAAAGG	420
QY	421	TGTGACATCTAAATATATCTGTTAACTTCTCTACGTTTGTGTTTACAGGCTTGCATTCA	480
DB	421	TGTGACATCTAAATATATCTGTTAACTTCTCTACGTTTGTGTTTACAGGCTTGCATTCA	480
QY	481	CCGAGTAGACGGGATTAATGAGCTGTACCGCATGTGATAGCGCTGTATAGTGCCAAAT	540
DB	481	CCGAGTAGACGGGATTAATGAGCTGTACCGCATGTGATAGCGCTGTATAGTGCCAAAT	540
QY	541	CATTTCAACACTCATATAGTCTTTTGTTCATCGGAAGCGATATGGAACGCAATCCAT	600
DB	541	CATTTCAACACTCATATAGTCTTTTGTTCATCGGAAGCGATATGGAACGCAATCCAT	600
QY	601	GACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCAGGATACCATAGATACACCC	660
DB	601	GACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCAGGATACCATAGATACACCC	660
QY	661	ACGACATACAGCATTAATGCTCATTAATACCATATGATGATGATGATGATGATGATGATG	720
DB	661	ACGACATACAGCATTAATGCTCATTAATACCATATGATGATGATGATGATGATGATGATG	720
QY	721	CTTAGGGATCTCTCTTTAGAGAGATGACAAACAGACAGCTTCAAGAAAGCAGAGTGA	780
DB	721	CTTAGGGATCTCTCTTTAGAGAGATGACAAACAGACAGCTTCAAGAAAGCAGAGTGA	780
QY	781	GAATGCCACCTCTGGTCTTCTCTGTTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTG	840
DB	781	GAATGCCACCTCTGGTCTTCTCTGTTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTG	840
QY	841	AGCCTTTCTGTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	900

DB	841	AGCCTTTCTGTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	900
QY	901	TATATTTGTACAAACATTTGCTGTCTAGTTTAAACATGTAAATGTTTGTATGATCTTTTC	960
DB	901	TATATTTGTACAAACATTTGCTGTCTAGTTTAAACATGTAAATGTTTGTATGATCTTTTC	960
QY	961	AAGACTCCATTTTGTGTTTAAAGGTAAACCTTGAATCTCATAGATTTGTCGATTTGTTG	1020
DB	961	AAGACTCCATTTTGTGTTTAAAGGTAAACCTTGAATCTCATAGATTTGTCGATTTGTTG	1020
QY	1021	TCCATTTTCAGTACGGTTCTGTAGACTGTAGTCTTGTGTGACAGCTCCGGCTTTAACACC	1080
DB	1021	TCCATTTTCAGTACGGTTCTGTAGACTGTAGTCTTGTGTGACAGCTCCGGCTTTAACACC	1080
QY	1081	CCAAATTTTCAAGATCTCACCAATCAAAATGCTGCTGCCCCCAATATATAGATGGGCCA	1140
DB	1081	CCAAATTTTCAAGATCTCACCAATCAAAATGCTGCTGCCCCCAATATATAGATGGGCCA	1140
QY	1141	GTTAATTCGCTCTAGCTTTTACTCTTTTAGACCTACTCTTTAGACAGTTAGACACCTGCT	1200
DB	1141	GTTAATTCGCTCTAGCTTTTACTCTTTTAGACCTACTCTTTAGACAGTTAGACACCTGCT	1200
QY	1201	ATGAGTTTCTCTTTTCTTGTTCAGCAAGTTACCTGTGTGTACCTTGAGAGTTGAGTTAAT	1260
DB	1201	ATGAGTTTCTCTTTTCTTGTTCAGCAAGTTACCTGTGTGTACCTTGAGAGTTGAGTTAAT	1260
QY	1261	TAGTAAAACGCAATTTTAAACCTTTTAAAGTTTAAATGCTATTCACAGAAATGACCCAG	1320
DB	1261	TAGTAAAACGCAATTTTAAACCTTTTAAAGTTTAAATGCTATTCACAGAAATGACCCAG	1320
QY	1321	TAAATAAATCCATCTGTAACCTTCAAAATTTCTTTTAAAGTAGCAAAATCATTT	1380
DB	1321	TAAATAAATCCATCTGTAACCTTCAAAATTTCTTTTAAAGTAGCAAAATCATTT	1380
QY	1381	AAATATTTGTAAGTTTCTTCAATTCGAAATTTGATGATACAGATCTCAAAGCTCCTCT	1440
DB	1381	AAATATTTGTAAGTTTCTTCAATTCGAAATTTGATGATACAGATCTCAAAGCTCCTCT	1440
QY	1441	GCCCATATCTCTCTTAACAAACGATAGTAACTTGCACACAGTTTGCATCTCTCGGG	1500
DB	1441	GCCCATATCTCTCTTAACAAACGATAGTAACTTGCACACAGTTTGCATCTCTCGGG	1500
QY	1501	GTTTTCATGCGCGGACTATGCGAGATTAATGATCAGATCGTCAATGAGACCTCTTTT	1560
DB	1501	GTTTTCATGCGCGGACTATGCGAGATTAATGATCAGATCGTCAATGAGACCTCTTTT	1560
QY	1561	ACAAACGGAATGGTTCTGAGTCACTTTTGCCTGGAATCTATGGAACCTTTTACCAAT	1620
DB	1561	ACAAACGGAATGGTTCTGAGTCACTTTTGCCTGGAATCTATGGAACCTTTTACCAAT	1620
QY	1621	TCTCTCAGACATGGCTCCGGAACTACCTCGCGGAAACATATCTTACTTCTATCTCGG	1680
DB	1621	TCTCTCAGACATGGCTCCGGAACTACCTCGCGGAAACATATCTTACTTCTATCTCGG	1680
QY	1681	TCTCTGTTGTTCTTACATCTATTAATTAATGATCGTCCCAAGGTTACT	1740
DB	1681	TCTCTGTTGTTCTTACATCTATTAATTAATGATCGTCCCAAGGTTACT	1740
QY	1741	TTTTTCAATTTTCGATGTTCTGTTTGTGAAACCTTTTCTTTTGTGATTCCTTCGAT	1800
DB	1741	TTTTTCAATTTTCGATGTTCTGTTTGTGAAACCTTTTCTTTTGTGATTCCTTCGAT	1800
QY	1801	GCTCATAGATTTGTTTATACGTTTAACTTTTCTTACTTCTTACTTCTTCTTCTTCT	1860
DB	1801	GCTCATAGATTTGTTTATACGTTTAACTTTTCTTACTTCTTACTTCTTCTTCTTCT	1860
QY	1861	TTCTACTTCTCAATTTTAAATTTAGTTTAAAGTTTAAATTTTGGCTTAAATCCATTT	1920
DB	1861	TTCTACTTCTCAATTTTAAATTTAGTTTAAAGTTTAAATTTTGGCTTAAATCCATTT	1920
QY	1921	AGTGAATCTTCCATGAAATTTGAGCTCAAAATATATCCATGAAATTTGAAATTTGCT	1980
DB	1921	AGTGAATCTTCCATGAAATTTGAGCTCAAAATATATCCATGAAATTTGAAATTTGCT	1980

Db 1921 AGTTGAATCTTCATGAAATTTGAGCTCAAAATATACCATGAAATTTGAAATTTGGTTC 1980
Qy 1981 TTAGTTCTATTTCTTCTGCTTGGTTCTTCTATTTTCTGTTAGAAATCCATTCCTACGAGA 2040
Db 1981 TTAGTTCTATTTCTTCTGCTTGGTTCTTCTATTTTCTGTTAGAAATCCATTCCTACGAGA 2040
Qy 2041 AAGGCAATGTTTGGCAATATACGTTGGCAATGAAGGCTATGCTTGGTACACCTCTCTT 2100
Db 2041 AAGGCAATGTTTGGCAATATACGTTGGCAATGAAGGCTATGCTTGGTACACCTCTCTT 2100
Qy 2101 CAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAAATGTTACTCTACACTTGAC 2160
Db 2101 CAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAAAATGTTACTCTACACTTGAC 2160
Qy 2161 CATTTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTATCTCTTTAGTTGAGTTT 2220
Db 2161 CATTTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTATCTCTTTAGTTGAGTTT 2220
Qy 2221 ATGATTTATTTGGTTTCAAAAGGCTTCATGACATTAATTTCTCTAAGCATCTCCAT 2280
Db 2221 ATGATTTATTTGGTTTCAAAAGGCTTCATGACATTAATTTCTCTAAGCATCTCCAT 2280
Qy 2281 GCTACCCATCATATGTACACAGCAAAACACACTCTCTCCATTTGCCGCTATGCAAG 2340
Db 2281 GCTACCCATCATATGTACACAGCAAAACACACTCTCTCCATTTGCCGCTATGCAAG 2340
Qy 2341 CTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGGTGACTTCTTTACTTGATGT 2400
Db 2341 CTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGGTGACTTCTTTACTTGATGT 2400
Qy 2401 TTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGGATATTCAGGCTATACCCG 2460
Db 2401 TTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGGATATTCAGGCTATACCCG 2460
Qy 2461 AGTGATAGCGCTTTTATAGTCCGATTCATCTCATACACATCTGAGTCTTTTGGTTT 2520
Db 2461 AGTGATAGCGCTTTTATAGTCCGATTCATCTCATACACATCTGAGTCTTTTGGTTT 2520
Qy 2521 TGAAGGGATATGGACAGCAAGCATCCATGATTCATACATGATGATCAATCTGGCTATAA 2580
Db 2521 TGAAGGGATATGGACAGCAAGCATCCATGATTCATACATGATGATCAATCTGGCTATAA 2580
Qy 2581 TGGTGCAGGATACCATACATACATACATACATACATACATACATACATACATACATACAT 2640
Db 2581 TGGTGCAGGATACCATACATACATACATACATACATACATACATACATACATACATACAT 2640
Qy 2641 CCATATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 2700
Db 2641 CCATATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 2700
Qy 2701 TCAAGGAGAAAGAAAGTGAAGTGTCAATGCTCACATGATTTCTTCATATGTTGCTCT 2760
Db 2701 TCAAGGAGAAAGAAAGTGAAGTGTCAATGCTCACATGATTTCTTCATATGTTGCTCT 2760
Qy 2761 TCTCGTGAATCTTATTAACCTTTCTATACATCTTGGTGGAAATTAACATGACTGCA 2820
Db 2761 TCTCGTGAATCTTATTAACCTTTCTATACATCTTGGTGGAAATTAACATGACTGCA 2820
Qy 2821 TAAATTTGATGCAAGTTTCAGACTTTTATGCTTAAATCTCTGATGATTTTAACTCA 2880
Db 2821 TAAATTTGATGCAAGTTTCAGACTTTTATGCTTAAATCTCTGATGATTTTAACTCA 2880
Qy 2881 ATTATATAATTTGCTGATGAAGTTTCAAAATTTGGACTAAATCTG 2925
Db 2881 ATTATATAATTTGCTGATGAAGTTTCAAAATTTGGACTAAATCTG 2925

RESULT 3
ID ABK89915
XX ABK89915 standard; DNA; 1889 BP.
AC ABK89915;
XX

DT 21-OCT-2002 (first entry)
XX
DE Gene encoding Arabidopsis thaliana dwf7 protein.
XX
KW Dwarf7; dwf7; plant cell; sterol composition; cholesterol;
KW plant regulatory defect; plant growth; plant; db.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 143..1709
FT /tag= a
FT /product= "dwf7"
FT exon 143..368
FT /tag= b
FT /number= 1
FT intron 369..735
FT /tag= c
FT /number= 1
FT exon 736..1041
FT /tag= d
FT /number= 2
FT intron 1042..1395
FT /tag= e
FT /number= 2
FT exon 1396..1706
FT /tag= f
FT /number= 3
PN US2002068822-A1.
XX
PD 06-JUN-2002.
XX
PP 02-FEB-2001; 2001US-00775879.
XX
PR 02-FEB-2000; 2000US-0179901P.
XX
PA (CHOE/) CHOE S.
PA (FELD/) FELDMANN K A.
XX
PI Choe S, Feldmann KA;
XX
DR WPI; 2002-582494/62.
DR P-PSDB; AAU99577.
XX
PT Novel isolated dwf7 polynucleotide for altering sterol composition of a
PT plant, by introducing polynucleotide into plant cell to produce
PT transformed plant cell and producing transgenic plant from transformed
PT cell.
XX
PS Claim 1; Fig 8; 53pp; English.
XX
CC The present invention relates to the isolation of dwarf7 (dwf7) mutants
CC and encoding polynucleotides that impart at least one dwf7 mutant
CC phenotype when expressed in a plant. The polynucleotide sequences
CC encoding the mutant dwf7 proteins are useful for producing transgenic
CC plants from transformed plant cells. The polynucleotide sequences are
CC useful for altering the sterol composition of a plant relative to the
CC wild-type plant. The transgenic plant has less cholesterol or increased
CC sterol production relative to the wild-type plant. The mutant sequences
CC are also useful for isolating or creating other mutant cell gene alleles,
CC and for detecting plant regulatory defects which can affect plant growth.
CC The present sequence encodes Arabidopsis thaliana dwf7 protein
XX
SQ Sequence 1889 BP; 466 A; 385 C; 352 G; 686 T; 0 U; 0 Other;
Query Match 31.6%; Score 924.4; DB 6; Length 1889;
Best Local Similarity 99.6%; Pred. No. 5.8e-206;
Matches 958; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
Qy 1 GTTTGGTATTTATTTGGATGTCAGAGAGCTTCATGACATTAAAGCTCTCTATAAGTATCT 60
Db 929 GTTTGGTATTTATTTGGATGTCAGAGAGCTTCATGACATTAAAGCTCTCTATAAGTATCT 988

Db 989 CCATGCCACCCATCATATCTACAACAGCAGATACACTCTCTCCATTTGCCGGTAAGTG 1048
Qy 121 TTTTCAGTTTGTCTCTTTAGTTCTTGTAAAGATTGGTAGCATTTAGTTCTTACCAG 180
Db 1049 TTTTCAGTTTGTCTCTTTAGTTCTTGTAAAGATTGGTAGCATTTAGTTCTTACCAG 1108
Qy 181 AAAAGACTTTGTGACAGCTGCTGTGTAATCTTCAATCACAATTTTGCAATTCCTTATCCATAA 240
Db 1109 AAAAGACTTTGTGACAGCTGCTGTGTAATCTTCAATCACAATTTTGCAATTCCTTATCCATAA 1168
Qy 241 AGTAACCAAGAGCTAGAAATATATATAATGTGAGCTGCAATTTACATATGTCCAGAG 300
Db 1169 AGTAACCAAGAGCTAGAAATATATATAATGTGAGCTGCAATTTACATATGTCCAGAG 1228
Qy 301 AGACTTCTGACTTAACAGAGTTAGATCTTTGTGTTTCTTCTGCTCTCGGACTGATT 360
Db 1229 AGACTTCTGACTTAACAGAGTTAGATCTTTGTGTTTCTTCTGCTCTCGGACTGATT 1288
Qy 361 GGAATAGCAGAGAGTTCTTTTATCTACTTCCCTGGAGTGATCTTTGGTTAATCCAAAGGA 420
Db 1289 GGAATAGCAGAGAGTTCTTTTATCTACTTCCCTGGAGTGATCTTTGGTTAATCCAAAGGA 1348
Qy 421 TGTGACATCTAATATCTGTAATCTTCTTACGTTTCTTACGTTTGTGTACAGGCTTGCA- TTC 479
Db 1349 TGTGACATCT- AATATTAATCTTGAATCTTCTTACGTTTGTGTGTACAGGCTTGCAATTC 1407
Qy 480 ACCGAGTAGACGGGATCTTAAGGCTGTACCGCATGTGATAGCGTG- TTATAGTGCCAA 538
Db 1408 ACCGAGTAGACGGGATCTTAAGGCTGTACCGCATGTGATAGCGTGTTTATAGTGCCAA 1467
Qy 539 TTTCAATTCACAACTCATATAGGTCTTTTGTTCATGAAGCGGATATGACGGCGAATCC 598
Db 1468 TTTCAATTCACAACTCATATAGGTCTTTTGTTCATGAAGCGGATATGACGGCGAATCC 1527
Qy 599 ATGACTGCAATCCATGGCAACATCTGGCCAGTAATGGGTGCAGGATACCATAGCATACCC 658
Db 1528 ATGACTGCAATCCATGGCAACATCTGGCCAGTAATGGGTGCAGGATACCATAGCATACCC 1587
Qy 659 ACACGACATACAAAGCACTACTATGGTCATTATACCATATGGATGGATGGATTTGGCT 718
Db 1588 ACACGACATACAAAGCACTACTATGGTCATTATACCATATGGATGGATGGATTTGGCT 1647
Qy 719 CTCTTAGGATCCTCTCTTAGAAGAGATGACAAAGACAGCTTCAAGAAAGCAGAGT 778
Db 1648 CTCTTAGGATCCTCTCTTAGAAGAGATGACAAAGACAGCTTCAAGAAAGCAGAGT 1707
Qy 779 GAGAAATGCCACTTGGGTTTGTCTCTGTTTGTCTGTTTGTGTTGTTGTTTCAAGTT 838
Db 1708 GAGAAATGCCACTTGGGTTTGTCTCTGTTTGTCTGTTTGTGTTGTTTCAAGTT 1767
Qy 839 TCAGGCTTTCTGTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCCA 898
Db 1768 TCAGGCTTTCTGTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCCA 1827
Qy 899 ATTATATTGTACAAACATTTGCTGCTAGTTTAAACATGTAAATGTTTGTATGATCTTT 958
Db 1828 ATTATATTGTACAAACATTTGCTGCTAGTTTAAACATGTAAATGTTTGTATGATCTTT 1887
Qy 959 GC 960
Db 1888 GC 1889

RESULT 5

AAC41897

ID AAC41897 standard; DNA; 1164 BP.

XX

AC AAC41897;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 33540.

XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.

XX 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264847P.
PR 22-JUN-2001; 2001US-030011P.
XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 421; 577bp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 846 BP; 222 A; 198 C; 170 G; 256 T; 0 U; 0 Other;

Query Match 11.9%; Score 347.2; DB 6; Length 846;
Best Local Similarity 72.4%; Pred. No. 6e-71;
Matches 508; Conservative 0; Mismatches 108; Indels 86; Gaps 1;

QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGCAGATATACGTGGCAATGAAGGCTAT 2081
DB |||||
DB 225 AGATGCAATTCCTACAAATGAAGCTATGCTTTGCAATGTTTGGCAATGAAGGCTAT 284
QY 2082 GCCTTGGTACACTCTCTTCCAGCTCTCTCTAGTATATGATCGACGATGGTTGGACCAA 2141
DB |||||
DB 285 GCCATGGTACACTCTCTTCCAACTGCTCCGAGAGTATGATTGAACGTGGTTGGACCAA 344
QY 2142 ATGTTACTCTACACTTGACCAATTCACCTGGTCTCTCTCTCTCTACATAGCTCTCTA 2201
DB |||||
DB 345 ATGTTTGTGCTAGCATAGGCGAATTCGGCTGGATTCTGTATTGTTTACATCGCCATCTA 404
QY 2202 TCTTGTGTTTGTAGTTGATGTTTATGATTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
DB |||||
DB 405 TCTGTTTTCGTTGAGTTGGTATTTATTTGATGTCACAGAGCTTCATGACATTAAGCC 464
QY 2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTTACAAACAGCAACACACTCTCTCC 2321
DB |||||
DB 465 TCTCTATAAGTATCTCCATGCCACCCATCATATCTACAAACAGCAACATCACTCTCTCC 524
QY 2322 ATTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGATCAATGG 2381
DB |||||
DB 525 ATTTGCC----- 531
QY 2382 TGACTTCTTTACTTGATGTTTTCGCGGTTTTCAGGGCTCGCATTCATCGCTGGACGGG 2441
DB |||||
DB 532 -----GGGCTTGCAATTCACCGAGTAGACGGG 558
QY 2442 ATACTTCAGGCTATACCGCAGTGCATGAGCTGTTTATAGTGCAGATTCAATCTCATACA 2501
DB |||||
DB 559 ATACTTCAGGCTGTACCGCATGTGATAGCGCTGTTTATAGTGCAGATTCAATTCACAACT 618
QY 2502 CATCTGAGCTTTTGTGTTGGAGGATATGACAGCAGCATCCATGATGATCATAT 2561
DB |||||
DB 619 CATATAGGCTTTTGTTCATGGAAGCGATATGACCGCGAATCATCATGACTGCATCCAT 678
QY 2562 GGTAACATCTGGCCTTAATGGGTGCGAGGATACCATACCATACCAACATACAAG 2621

DB 679 GGCAACATCTGCGCAGTAATGGGTGAGATACCATACATACACACAGACATACAAG 738
QY 2622 CATAACTATGTCATATATACCATATGATGGATGGATGTTGGCTCTCTTATGGTCTCT 2681
DB |||||
DB 739 CATAACTATGTCATATATACCATATGATGGATGGATGTTGGCTCTCTTATGGGATCT 798
QY 2682 TTAGCAGAAAAAGACACAGTTTCAAGGAGAAAGAAAAGTGAAG 2723
DB |||||
DB 799 CTCTTAGAAGAAGATGACACAAAGACAGCTTCAAGAAAGCA 840

RESULT 8
ABX15834
ID ABX15834 standard; cDNA; 1447 BP.
XX
AC ABX15834;
XX
DT 31-MAR-2003 (first entry)
XX
DE cDNA encoding soybean sterol C5 desaturase protein #2.
XX
KW Corn; wheat; rice; soybean; plant; gene; ss; sterol metabolism;
KW sterol delta 7; reductase; sterol C5 desaturase.
XX
OS Glycine max.
XX
PN US6465717-B1.
XX
PD 15-OCT-2002.
XX
PF 19-NOV-1999; 99US-00443041.
XX
PR 20-NOV-1998; 98US-0109283P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Famodu OO, Rafalaki JA;
XX
DR WPI; 2003-147075/14.
DR P-PSDB; ABG73990.
XX
PT Novel polynucleotide encoding sterol metabolism enzyme useful for
PT producing transgenic plant, has nucleotide sequence encoding the
PT polypeptide having sterol delta-7 reductase activity.
XX
PS Disclosure; Col 57-58; 39pp; English.
XX
CC This invention relates to novel isolated polynucleotide encoding sterol
CC metabolism enzyme. The nucleotide sequence of the invention is useful for
CC transforming a cell by introducing the sequence into a cell. The
CC sequences may also be useful for producing a transgenic plant, by
CC transforming a plant cell with the cDNA sequence and regenerating a
CC transgenic plant from the transformed plant cell. The nucleotide sequence
CC is useful for obtaining a nucleic acid fragment encoding all or a
CC substantial portion of the amino acid sequence encoding a sterol delta-7
CC reductase or a sterol-C5 desaturase polypeptide. Probes derived from the
CC nucleotide sequence of the invention may be useful for physical mapping.
CC The present sequence represents a cDNA sequence encoding a sterol
CC metabolism enzyme of the invention
XX
SQ Sequence 1447 BP; 444 A; 283 C; 294 G; 426 T; 0 U; 0 Other;

Query Match 7.0%; Score 203.4; DB 8; Length 1447;
Best Local Similarity 61.3%; Pred. No. 3.4e-37;
Matches 399; Conservative 0; Mismatches 166; Indels 86; Gaps 1;

QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGCAGATATACGTGGCAATGAAGGCTAT 2081
DB |||||
DB 316 AGATGCTATCTCCTCTCAAGAGCCATGCTCTTGCAGATATCTGTTGCTATGAAGCCAT 375
QY 2082 GCCTTGGTACACTCTCTTCCAGCTGTCTCTGAGTATATGATCGACATGGTTGGACCAA 2141
DB |||||

DT 22-APR-2004 (first entry)
 XX Rice isoprenoid biosynthesis-associated cDNA #144.
 XX
 DE Rice; isoprenoid biosynthesis; ss; gene; plant; isopentenyl diphosphate;
 KW IPP; dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase;
 KW gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone;
 KW phyloquinone; mevalonate pathway; phytosterol; brassinosteroid;
 KW ubiquinone; monoterpene; sesquiterpene; protein prenylation; chlorophyll;
 KW haeme; yield.
 XX
 XX Oryza sativa.
 OS
 XX
 XX US2004010815-A1.
 XX
 XX 15-JAN-2004.
 XX
 XX 26-SEP-2002; 2002US-00259194.
 XX
 XX 26-SEP-2001; 2001US-0325277P.
 PR 04-APR-2002; 2002US-0370620P.
 PR 04-APR-2002; 2002US-0370743P.
 XX
 XX (LANG/) LANGE B M.
 PA (GHAS/) GHASSEMIAN M.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (MOUG/) MOUGHANER T.
 PA (PROV/) PROVANT N.
 PA (RICK/) RIQUE D.
 PA (ZHUT/) ZHU T.
 XX
 XX Lange BM, Ghassemian M, Briggs SP, Cooper B, Glazebrook J;
 PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provant N, Ricke D;
 PI Zhu T;
 XX
 XX WPI; 2004-090562/09.
 DR P-PSDB; ADI45357.
 DR
 XX
 XX New isolated polynucleotides and polypeptides associated with isoprenoid
 PT synthesis in plants, useful for producing transgenic plants, for targeted
 PT gene disruption, as well as markers or probes.
 XX
 XX Claim 1; SEQ ID NO 287; 117pp; English.
 XX
 CC The invention relates to a polynucleotide (or its complement, protein
 CC encoding fragment or reverse complement), comprising a nucleotide
 CC sequence encoding a polypeptide comprising an amino acid sequence
 CC involved in or associated with the biosynthesis of isoprenoids in a rice
 CC plant. Also included are an isolated polypeptide involved in or
 CC associated with the biosynthesis of isoprenoids in a plant, an expression
 CC cassette comprising the polynucleotide, a host cell comprising the
 CC expression cassette, and a transgenic plant comprising the expression
 CC cassette. The polypeptides and polynucleotides include those associated
 CC with the biosynthesis of isopentenyl diphosphate (IPP) and dimethylallyl
 CC alcohol (DMAPP), the biosynthesis of short-chain plastid
 CC prenyltransferases, the biosynthesis of gibberellins, the biosynthesis of
 CC carotenoids and/or abscisic acids, the biosynthesis of tocopherols,
 CC phytoquinone and/or phyloquinone biosynthesis, the mevalonate pathway,
 CC phytosterol and brassinosteroid metabolism, biosynthesis of ubiquinone,
 CC biosynthesis of monoterpenes and sesquiterpenes, protein prenylation, and
 CC biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat
 CC and corn homologues of some of the rice polynucleotides. The
 CC polynucleotides are useful for producing transgenic plants, where the
 CC genome is augmented by a nucleic acid molecule of the invention, or in
 CC which the corresponding gene has been disrupted, e.g. to result in a
 CC loss, a decrease or an alteration in the function of the product encoded
 CC by the gene. The plants may also have increased yields and/or produce a
 CC better quality product than the corresponding wild-type plant. The

CC nucleic acid molecules are useful for targeted gene disruption, as well
 CC as markers and probes. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from USPIO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040010815. The present sequence
 CC is a Rice isoprenoid biosynthesis-associated cDNA of the invention.
 XX
 XX Sequence 833 BP; 199 A; 226 C; 193 G; 215 T; 0 U; 0 Other;
 SQ
 Query Match 6.5%; Score 189.4; DB 12; Length 833;
 Best Local Similarity 59.3%; Pred. No. 5.3e-34;
 Matches 393; Conservative 0; Mismatches 191; Indels 79; Gaps 1;
 QY 2023 GAATCCATTTCCTACGAGAAAGCAATGCTTTTGCAATATATAGTGGCAATGAAGGCTATG 2082
 DB |||||
 QY 230 GATTCTATACCTACCAATCGAGCTATGAAGAGCAATTAATTTGGCATCAAGGCTATG 289
 DB |||||
 QY 2083 CCTTGGTACACTCTTTCTCCAGCTGTCTCTGTAGTATATATGATCGAGATGTTGGACAAA 2142
 DB |||||
 QY 290 CCTCTCTATTGTGCCCTTCCAACTTATCTGAGTACATGGTTGAGAAATGGATGGACACAG 349
 DB |||||
 QY 2143 TGTACTCTACACTTGCACATTTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTAT 2202
 DB |||||
 QY 350 TGTATATTAATATCATGTAAGTGTGGTGGCAATGTACTGGTTTATCTGGCTTTATAT 409
 DB |||||
 QY 2203 CTGTGTTTGTAGTTGAGTTTATGATTTTATTGGGTTTCAAAAGAGCTTTCATGACATTAATTT 2262
 DB |||||
 QY 410 CTATCTTTGTTGAGTTTGGAAATTTATCGGATGCACAGAGATTGTCATGACATAAGCCA 469
 DB |||||
 QY 2263 CTCTATAAGCATCTCCATGCTACCCATCATATGTATCAACAAGCAAAACACATCTCTCCA 2322
 DB |||||
 QY 470 TTGTACAAGTACCTGCACATACCAACCATATTTTCAACAAGGAGAAATACCCCTATCACCA 529
 DB |||||
 QY 2323 TTTGGGGTATGTCAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGGT 2382
 DB |||||
 QY 530 TTTCGCTCTCTTTTACCTGATGTTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGACGGA 534
 DB |||||
 QY 2383 GACTCTCTTTTACCTGATGTTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGACGGA 2442
 DB |||||
 QY 535 -----AGTTTCAGGAGCTAGCATTCATCCATCCACTGGATGGA 570
 DB |||||
 QY 2443 TACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTGGGATTCATCTCATTAACAC 2502
 DB |||||
 QY 571 TTTTTCGAGCCATACCGCATGTTGTTGCGCTCTACCTTATCCCAACACACATTCAGGACAC 630
 DB |||||
 QY 2503 ATCTGAGCTTTTGTGTTTGGAGGATATGACAGCAGCATCCATGATGTCATACATG 2562
 DB |||||
 QY 631 ACAATTGCTCTCTTGTTCATAGAGCGCGTGTGGACAACTAACATCCATGACTGCATTCACG 690
 DB |||||
 QY 2563 GTAAACATCTGGCTTATATATGGGTGAGGATACCATACCATACCAACATACCAAGC 2622
 DB |||||
 QY 691 GCAGGTTTGGCGGTGATGTTGCGTGTGCTATACACCATTCACCATACCAATCCGTC 750
 DB |||||
 QY 2623 ATAACTATGGTCAATTATACCATATGATGATGAGATGGATGTTGGCTCTCTTATGGTTCCTT 2682
 DB |||||
 QY 751 ACAACTATGGCCACTACACCGTGTGGATGCTGGATGTTGCGCACCCCTTCGAGAGCCAG 810
 DB |||||
 QY 2683 TAG 2685
 DB |||||
 QY 811 AAG 813
 DB |||||

RESULT 11
 ADI45599
 ID ADI45599 standard; cDNA; 1135 BP.
 XX
 XX ADI45599;
 AC
 XX 22-APR-2004 (first entry)
 DT Wheat isoprenoid biosynthesis-associated cDNA #57.
 DE Wheat; isoprenoid biosynthesis; ss; plant; isopentenyl diphosphate; IPP;
 KW

dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phyloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monoterpene; sesquiterpene; protein prenylation; chlorophyll; haeme; yield.

Triticum aestivum.

US2004010815-A1.

15-JAN-2004.

26-SEP-2002; 2002US-00259194.

26-SEP-2001: 2001US-0325277P.

04-APR-2002; 2002US-0370620P.

04-APR-2002; 2002US-0370743P.

(LANG/) LANGE B M.

(GHAS//) GHASSEMIAN M.

(BRIG//) BRIGGS S P.

(COOP/) COOPER B.

(GLAZ//) GLAZEBROOK J.

(GOFF//) GOFF S A.

(KATA/) KATAGIRI F.

(KREP//) KREPS J.

(MOUG/) MOUGHAMER T.

(PROV//) PROVART N.

(RICK/) RICE D.

(ZHUT/) ZHU T.

Lange BM, Ghassemlan M, Briggs SP, Cooper B, Glazebrook J;
Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;
Zhu T;

WPI; 2004-090562/09.

New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.

Disclosure: SEQ ID NO 530: 117pp; English:

The invention relates to a polynucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression cassette comprising the polynucleotide, a host cell comprising the expression cassette, and a transgenic plant comprising the expression cassette. The polypeptides and polynucleotides include those associated with the biosynthesis of isopentenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid prenyltransferases, the biosynthesis of gibberellins, the biosynthesis of carotenoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phytylquinone biosynthesis, the mevalonate pathway, phytylsterol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of monoterpenes and sesquiterpenes, protein prenylation, and biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polynucleotides. The polynucleotides are useful for producing transgenic plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a better quality product than the corresponding wild-type plant. The nucleic acid molecules are useful for targeted gene disruption, as well as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040010815. The present sequence is a Wheat Isoprenoid Biosynthesis-associated cDNA of the invention.

```
PR 20-NOV-1998; 98US-0109283P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Famodu OO, Rafalski JA;
XX
XX WPI; 2003-147075/14.
XX P-PSDB; ABG73991.
XX
XX Novel polynucleotide encoding sterol metabolism enzyme useful for
XX producing transgenic plant, has nucleotide sequence encoding the
XX polypeptide having sterol delta-7 reductase activity.
XX
XX Disclosure; Col 59-62; 39pp; English.
XX
XX This invention relates to novel isolated polynucleotide encoding sterol
XX metabolism enzyme. The nucleotide sequence of the invention is useful for
XX transforming a cell by introducing the sequence into a cell. The
XX sequences may also be useful for producing a transgenic plant, by
XX transforming a plant cell with the cDNA sequence and regenerating a
XX transgenic plant from the transformed plant cell. The nucleotide sequence
XX is useful for obtaining a nucleic acid fragment encoding all or a
XX substantial portion of the amino acid sequence encoding a sterol delta-7
XX reductase or a sterol-C5 desaturase polypeptide. Probes derived from the
XX nucleotide sequence of the invention may be useful for physical mapping.
XX The present sequence represents a cDNA sequence encoding a sterol
XX metabolism enzyme of the invention
XX
XX Query Match 6.4%; Score 188; DB 8; Length 1210;
XX Best Local Similarity 59.8%; Pred. No. 1.3e-33;
XX Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;
XX
XX 2022 AGAATCCATCTCCACGAGAAAGCAATGCTTTTGCMAATATACGTGGCAATGAAGGCTAT 2081
XX |||||
XX 188 AGATGCTGTCCTACAGTAGAGCTATGAAGAGCAATAATTTGTCATCAAGGCTAT 247
XX |||||
XX 2082 GCCTGGTACACTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141
XX |||||
XX 248 GCCTTTCTACTGTGCTCTTCCGTCGTATCTGAGCACAATGATTGAGAGTGGATGGAC 307
XX |||||
XX 2142 ATGTTACTCTACACTTGCATTTCAACTGGTTCCTCTCTCTACATAGCTCTCTA 2201
XX |||||
XX 308 GTGTTTCTTATATCAGCGAGTGGTGGCCATGTATATCTATCTGTCTCTATA 367
XX |||||
XX 2202 TCTGTTTGTAGTTGATGATTTATTGGGTTCAAGAGCTTCATGACATTAATTT 2261
XX |||||
XX 368 TCTCATCTTTGTGGAGTTCGGAATTTACTGGATGCACAGAGTTGTCATGACATAAGCC 427
XX |||||
XX 2262 TCTCTATAGCATCTCCATGCTACCCATCATATGATGATACACAGCAACACACTCTCTCC 2321
XX |||||
XX 428 ACTATACAGCACCCTACATGCAACCCACCACATTTTACAAACAGGAGTAACCTATCACC 487
XX |||||
XX 2322 ATTTGCGGATGTCMAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381
XX |||||
XX 488 ATTTG----- 492
XX
XX 2382 TGACTTCTTATCTTGATGTTTTCGGGTTTTCAGGGCTCGCATTCATCCGTGGACGGG 2441
XX |||||
XX 493 -----CTGGACTAGCATTTCCATTCCTATTCGAGCGG 521
XX
XX 2442 ATACTTCAGGCTATACGCGATGATAGCGCTGTTTATAGTGGCGATTCATCTCAATCA 2501
XX |||||
XX 522 ATACTCGAAGCCATATGCGACGTTGTTGCTCTCTCTCTCTCCGATGCACTTCAGGACG 581
XX |||||
XX 2502 CATCTGAGTCTTTGTTTGGAGGATGATGACAGCAGCATCCATGATTTGCATACAT 2561
XX |||||
XX 582 CAAATTGCTCTCTATTCATAGAGCGGTGTGACGGCAACATCCACGACTGCATCCAC 641
XX |||||
XX 2562 GGTAAATCTGGGCTATAATGGGTGAGGATACCATACCATACCATACCATACCATCAAG 2621
XX |||||
XX 642 GCGAAGATCTGGCGGTGATGGCGCGGCTACCATACCATACCATACCATACCATACCG 701
XX |||||
```

```
QY 2622 CATRACTATGGTCATTATACCATATGGATGGACTGGATGTTGGCTCTCT 2671
DB |||||
702 CACAACTATGGCCACTACACCGTGGATGGACTGGCTGTTGGACCCCT 751
|||
```

RESULT 13

```
AD119008
ID AD119008 standard; cDNA; 1210 BP.
XX
XX AC AD119008;
XX
XX DT 15-APR-2004 (first entry)
XX
XX DE Wheat sterol-C5-desaturase cDNA #2.
XX
XX KW Transcription factor; genetic mapping; plant breeding;
XX sterol-C5-desaturase; wheat; gene; ss.
XX
XX OS Triticum aestivum.
XX
XX FH Key Location/Qualifiers
XX CDS 54..761
XX FT /tag= a
XX FT /product= "Sterol-C5-desaturase"
XX FT /partial
XX FT /note= "No start and stop codon"
XX
XX PN US2003229914-A1.
XX
XX PD 11-DEC-2003.
XX
XX PF 21-AUG-2002; 2002US-00224880.
XX
XX PR 20-NOV-1998; 98US-0109283P.
XX PR 19-NOV-1999; 99US-00443041.
XX
XX PA (FAMO/) FAMODU O O.
XX PA (OROZ/) OROZCO E M.
XX PA (RAFA/) RAFALSKI J A.
XX PA (SHEN/) SHEN J B.
XX
XX PI Famodu OO, Orozco EM, Rafalski JA, Shen JB;
XX
XX WPI; 2004-052051/05.
XX P-PSDB; AD119009.
XX
XX New polynucleotide encoding a transcription factor polypeptide, useful in
XX genetic mapping for plant breeding.
XX
XX Claim 2; SEQ ID NO 29; 43pp; English.
XX
XX The invention relates to a polynucleotide which encodes a transcription
XX factor. The nucleic acid fragment is useful in genetic mapping for plant
XX breeding. The present sequence is sterol-C5-desaturase cDNA.
XX
XX Sequence 1210 BP; 323 A; 288 C; 293 G; 305 T; 0 U; 1 Other;
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Query Match 6.4%; Score 188; DB 12; Length 1210;
Best Local Similarity 59.8%; Pred. No. 1.3e-33;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;
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QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGCMAATATACGTGGCAATGAAGGCTAT 2081
DB |||||
188 AGATGCTGTCCTACAGTAGAGCTATGAAGAGCAATAATTTGTCATCAAGGCTAT 247
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2082 GCCTGGTACACTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141
DB |||||
248 GCCTTTCTACTGTGCTCTTCCGTCGTATCTGAGCACAATGATTGAGAGTGGATGGAC 307
|||
2142 ATGTTACTCTACACTTGCATTTCAACTGGTTCCTCTCTCTACATAGCTCTCTA 2201
DB |||||
308 GTGTTTCTTATATCAGCGAGTGGTGGCCATGTATATCTATCTGTCTCTATA 367
|||
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Qy		2202	TCTTGTTTATTAGTTGAGTTATGATTTATGGGTTTCACAAAGAGCTTCATGACATTAAATT	2261
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Qy		2262	TCTCTAATAGCATCTCCATGCTACCCATCATATGTACAACAAGCAAAACACACTCTCTCC	2321
Db		428	ACTATACAAGCACCTCATATGCAACCACCACTTTTACAACAAGGAGAATACCCCTATCACC	487
Qy		2322	ATTTGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG	2381
Db		488	ATTTG-----	492
Qy		2382	TGACTTCTTTACTTGTATGTTTTTCGGGTTTTCAGGGCTCGCAITCCATCCGCTGGACGGG	2441
Db		493	-----CTGGACTAGCAITTCATCCATGGACGGG	521
Qy		2442	ATACTTCAGGCTATPACCGCAGTGATAGCGTGTTTATAGTGGCGATTCAATCTCATNAACA	2501
Db		522	ATACTGCAGGCATATCGCAGTGATTTGCTGTCTCTTCTCCGATGCACTTCAGGACG	581
Qy		2502	CATCTGAGTCTTTTGTTTTTTGGGAAGGATATGGACAGCAATCCATGATGCATACAT	2561
Db		582	CACATTGCTCTCTTAITCATAGAGCGGCTGTGGACGCCAAAACATCCACGACTGCATCCAC	641
Qy		2562	GGTAAACATCTGGGCTATAATGGGTGCAGGATACCATACCATACACCATCAACATACAAG	2621
Db		642	GGCAGATCTGGCCGGTGATGGGCCGCGTCAACACCAITCAACCAACAGGTACCGG	701
Qy		2622	CATAACTATGGTCAATTATACATATGATGGACTGGATGTTGGCTCTCT	2671
Db		702	CACAACATATGGCACTACACCGTGTGATGGACTGGCTGTTTGGACACCT	751

CC	sequences may also be useful for producing a transgenic plant, by
CC	transforming a plant cell with the cDNA sequence and regenerating a
CC	transgenic plant from the transformed plant cell. The nucleotide sequence
CC	is useful for obtaining a nucleic acid fragment encoding all or a
CC	substantial portion of the amino acid sequence encoding a sterol delta-7
CC	reductase or a sterol-C5 desaturase polypeptide. Probes derived from the
CC	nucleotide sequence of the invention may be useful for physical mapping.
CC	The present sequence represents a cDNA sequence encoding a sterol
CC	metabolism enzyme of the invention
XX	
SQ	Sequence 911 BP; 222 A; 214 C; 217 G; 258 T; 0 U; 0 Other;
	Query Match 6.4%; Score 187; DB 8; Length 911;
	Best Local Similarity 59.8%; P-red. No. 2e-33;
	Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps 1.
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DB	74 GATGCCATCCCAACAAATGAAGCTATGAAGAAGCAAAATAGCTGTAGCATCCCAAGGCTATG 133
QY	2083 CCTTGGTACACTCTTCTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2142
DB	134 CCTTTTACTGTGCTCTTCCAACCTTATCTGAGTATATGATCGAGAGTGTGATGGAACCCGG 193
QY	2143 TGTTACTCTACACTTGACCAATTTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTAT 2202
DB	194 TGTTACTTTAATATCAGCGAAATGGGTTTTCTGCATACCTTTGTTTATATGGCTATGTAT 253
QY	2203 CTTGTTTTAGTTAGTATTAATGATTTATGGGTTTCAAAAGAGCTTCATGACATTAATTT 2262
DB	254 CTCAATTTTGTGGAGTTTGGAAATTTACTGGATGTCACAGAGAGTTGATGACATAAAGCCA 313
QY	2263 CTCATAAGCATCTCCATCGTACCCCATCATGTACAACAAGCAAAACACACTCTCTCCA 2322
DB	314 CTATACAAACATCTGATATGGACCCACCATATTTACACACAGGAGAACACTTGTCTCCG 373
QY	2323 TTTTCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCGAAGAGCTTGATCAATGGT 2382
DB	374 TTTGCT-----TGAGCTCGGTTTTTCAACCAGTGGATGGTA 378
QY	2383 GACTTCTTTACTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCATTCATCCGCTGGACGGGA 2442
DB	379 -----TGAGCTCGGTTTTTCAACCAGTGGATGGTA 407
QY	2443 TACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTCGGGATTCATCTCATAAACAC 2502
DB	408 TTTCTGAAGCGATACCGCATGTGCTTGCGCTCTTCTCCTCTCCCAAGCGACTTCAGGACGC 467
QY	2503 ATCTGAGTCTTTTGTGTTTGGAAAGGATATGACAGCAGCATCCATGATTTGCATACATG 2562
DB	468 ACATCGCTCTCGTGTTCCTTGGAGGGCGGTGTGAACGCAAAACATCCACGACTCGATTCACG 527
QY	2563 GTAAACATCTGGGCTATAATGGGGTGCAGGATACCATACCATACACATAACAACATACAAGC 2622
DB	528 GCAAGGATATGGCCAGTATGGGGCGTGGGTATACACACCATCCACCATACGACTTACGCC 587
QY	2623 ATAACTATGGTCATATATACATATGGATGGACTGGATGTTGGCTCTCT 2671
DB	588 ACAACTATGGCACTACACCGTCTGGATGGACTGGATGTTGGTAGCGT 636

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
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 (without alignments)
 12273.741 Million cell updates/sec
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 Perfect score: 2925
 Sequence: 1 gtttggtatttattggtgc.....tcaaatgttgactaaatctg 2925

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 41078325 seqs, 23393541228 residues
 Total number of hits satisfying chosen parameters: 82156650
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_est3:
 4: gb_hic:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_est7:
 9: gb_gsa1:
 10: gb_gsa2:
 11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	355.4	12.2	940	CL460967	CL460967 SAIL 1124
2	336	11.5	772	CD834215	BN45_040P
3	321	11.0	963	CL516186	SAIL_914
4	299.4	10.2	328	BH846526	SALK_0085
5	285.6	9.8	700	BH956101	odg94b06
6	284.4	9.7	326	CB255600	36-E01842
7	283.8	9.7	1016	CL488421	SAIL 508
8	281.6	9.6	749	CD822918	BN25_047B
9	278.4	9.5	327	BZ384971	SALK_1362
10	265.4	9.1	482	CD823327	BN25_048G
11	249.8	8.5	644	CD834242	BN45_041B
12	228.4	7.8	869	7 CK264500	EST710578
13	228.4	7.8	920	7 CK269990	EST716068
14	227	7.8	924	7 CK264499	EST710577
15	226.6	7.7	753	7 CN731853	24RDNH_U
16	225.6	7.7	812	7 CO817044	FA_Sea000
17	225.4	7.7	683	7 CN730353	24RDNH_U
18	222	7.6	900	8 DR942311	EST113385
19	210.2	7.2	898	8 DR934644	EST112618
20	210	7.2	828	6 CB979536	CAB40007
21	202.8	6.9	832	5 BW687757	BM685027
22	202	6.9	837	8 DR942312	EST113385

C 23	197.2	6.7	920	8	DR580137	DR580137 WS00753.C
C 24	197.2	6.7	927	8	DR584230	DR584230 WS0335.C2
C 25	196.6	6.7	820	8	DR089207	DR089207 RTAL1 7 E
26	194.6	6.7	508	6	CB240394	CB240394 PopS0037
27	187.6	6.4	843	7	CN130796	CN130796 RHO1 43
C 28	185.2	6.3	834	8	DR931343	DR931343 EST112288
C 29	184.8	6.3	720	6	CD436598	CD436598 EL01N0360
C 30	184.8	6.3	757	6	CD434877	CD434877 EL01N0329
C 31	183.8	6.3	727	6	CA252633	SCVPL1114
C 32	183.4	6.3	846	8	DR469736	DR469736 WS00948.B
C 33	183.2	6.3	608	6	CF272845	CF272845 EST3051.Z
C 34	183.2	6.3	774	8	DR934543	DR934543 EST112618
C 35	183	6.3	861	8	DR469256	DR469256 WS00947.B
36	179.6	6.1	825	10	CL957247	CL957247 OeIFCC000
37	179.6	6.1	1080	8	CDX09651	RECm0308
38	178.8	6.1	798	8	DR109676	DR109676 RTS1 4 A0
39	178.4	6.1	644	6	CF227924	CF227924 PraxM0006
40	177.4	6.1	844	7	CK251357	CK251357 EST734994
41	175.8	6.0	721	7	CN884525	CN884525 O10811AAS
C 42	175.6	6.0	732	6	CD938892	CD938892 OV.111G01
C 43	175.2	6.0	815	5	BW685027	BW685027 BM685027
44	173.6	5.9	742	8	CK659607	CK659607 P001032G0
45	172.6	5.9	416	7	CN493842	CN493842 Mdfw2007d

ALIGNMENTS

RESULT 1
 CL460967
 LOCUS
 DEFINITION
 SAIL 1124_H08.v1 SAIL Collection Arabidopsis thaliana genomic clone
 SAIL 1124_H08.v1, genomic survey sequence.
 ACCESSION
 CL460967.1 GI:45863872
 VERSION
 GSS.
 KEYWORDS
 Arabidopsis thaliana (thale cress)
 SOURCE
 Arabidopsis thaliana
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE
 1 (bases 1 to 940)
 Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
 Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D.,
 Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
 Mittel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A.
 A high-throughput Arabidopsis reverse genetics system
 Plant Cell 14 (12), 2985-2994 (2002)
 12468722
 TITLE
 JOURNAL
 PUBLISHED
 COMMENT
 Contact: Sessions A
 Applied Trait Genetics
 Syngenta Biotechnology Inc.
 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
 Email: allen.sessions@syngenta.com
 Syngenta Stock Number CS841870; T-DNA left border flanking sequences of
 Arabidopsis thaliana insertion library (SAIL) lines are available
 through the Arabidopsis Biological Resource Center (ABRC).
 Sequences represent a pool of amplified genomic regions and not
 single contiguous sequences.
 Class: TDNA tagged.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /acctype="Columbia"
 /db_xref="taxon:3702"
 /clone="SAIL_1124_H08.v1"
 /note="T-DNA left border sequences were isolated using a
 modified TAIL-PCR strategy"

Query Match 12.2%; Score 355.4; DB 10; Length 940;

Best Local Similarity 99.7%; Pred. No. 3 5e-70; Mismatches 356; Conservative 0; Indels 0; Gaps 0;

QY 1319 TTTAAATAATCATCGTAACCTCCACCTTCAAAATCTTTTAAAGTAGCAATCAT 1378

Db 73 TGTAAATAATCATCGTAACCTCCACCTTCAAAATCTTTTAAAGTAGCAATCAT 132

QY 1379 TTAATATTTGTAAGTTTGTCTCAATTCGAAATTTGTAGCTACAGATCTCAAGCTCTCTCCG 1438

Db 133 TTAATATTTGTAAGTTTGTCTCAATTCGAAATTTGTAGCTACAGATCTCAAGCTCTCTCCG 192

QY 1439 TTGGCCATATCTCTCTAAACAAACGATAGTAACCTTTGACCAACAGATTTGACTTCTCGG 1498

Db 193 TTGGCCATATCTCTCTAAACAAACGATAGTAACCTTTGACCAACAGATTTGACTTCTCGG 252

QY 1499 CGGTTTCATGGCGGCGACTATGGCAGATTAATATGATGATCGTCAATGAGACCTCTTT 1558

Db 253 CGGTTTCATGGCGGCGACTATGGCAGATTAATATGATGATCGTCAATGAGACCTCTTT 312

QY 1559 TTACACCGAATGGTTCTCAGTCACCTTTTGGCGGTGAATCTATGGGACCTTTACCACA 1618

Db 313 TTACACCGAATGGTTCTCAGTCACCTTTTGGCGGTGAATCTATGGGACCTTTACCACA 372

QY 1619 TTTCCTCCAGACATGCTCCGGAATACCTCGCGGAAACATATCTTCTATCTC 1675

Db 373 TTTCCTCCAGACATGCTCCGGAATACCTCGCGGAAACATATCTTCTATCTC 429

RESULT 2

CD834215

LOCUS

DEFINITION

CD834215

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 772)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbioigen.fr>).

FEATURES

source

1..772

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet Neuf"

/db_xref="taxon:3708"

/clone="BN45040P13"

/tissue type="seed"

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ORIGIN

Query Match 11.5%; Score 336; DB 6; Length 772;

Best Local Similarity 75.7%; Pred. No. 9.3e-66;

Matches 471; Conservative 0; Mismatches 65; Indels 86; Gaps 1;

QY 2022 AGATCCATCTTACGGAAGGCAATGCTTTTGGCAATATACGTGCAATGAAGGCTAT 2081

Db 237 AGATTTCTTCTTACGAAGGCAATGATTCGCAATATACATGTGGCAGTGAAGGAT 296

QY 2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141

Db 297 GCCTTGGTATACACTTTTCCCAACTGTCTCTGAGTATATGATCGAGCGTGTGGACCAA 356

QY 2142 ATGTTACTCTACACTTGACCAATTTCAACTGGTTCCTCTGTTTCTCTATACAGCTCTCTA 2201

Db 357 ATGTTACTCTACACTTGACCAATTCARCTGGTTCCTCTGTTTGTATACATCGTCTCTA 416

QY 2202 TCTCTGTTTGTAGTTGATTTATGATTTATTTGGGTTTCAAAAGAGCTTTCATGACATTAAT 2261

Db 417 TCTCTTATAGTTGATTTGATGATTTGTTTCAAAAGGCTTTCATGACATTAAT 476

QY 2262 TCTCTATAGCATCTCTCATGCTACCCATCATATGTAACAAGCAAAACACACTCTCTCC 2321

Db 477 TCTCTATAGCATCTCTCATGCTACCCATCATATGTAACAAGCAAAACACACTCTCTCC 536

QY 2322 ATTTCGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCGAAGCTTGTATCAATGG 2381

Db 537 ATTTG----- 541

QY 2382 TGAGTCTTCTTACTTGATGTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGG 2441

Db 542 -----CTGGGTTTGGTCCCATCCATTTGGACGGG 570

QY 2442 ATACTTCAGGCTATACCCACGATGATAGCGCTGTTTATAGTCCGATTCATCTCATAA 2501

Db 571 ATACTTCAGGCTGACCAATGATGATGCTCTGTTTCATAGTCCGCTTCATCTCATACG 630

QY 2502 CATCTGAGTCTTCTGTTTTCGGAAGGATATGACAGCAAGCATCCATGATTCATACAT 2561

Db 631 CATATGAGTCTTCTGTTTTCGGAAGGATATGACAGCAAGCATCCATGATTCATACAT 590

QY 2562 GGTAACTATCTGCGCTTATATGCGTGCAGATACCATACATACACCAACATCAAG 2621

Db 691 GGTAACTATCTGCGCTTATATGCGTGCAGATACCATACATACCAACCACTACTAAATAAG 750

QY 2622 CATAACTATGTCATTATACCA 2643

Db 751 CATAACTATGTCATTATACCA 772

CL516186

963 bp

DNA

linear

GSS 01-APR-2004

SAIL 914_D07.v2 SAIL Collection Arabidopsis thaliana genomic clone

SAIL_914_D07.v2, genomic survey sequence.

CL516186

GI:46013506

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 963)

Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B., Mitrel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.

A high-throughput Arabidopsis reverse genetics system

Plant Cell 14 (12), 2985-2994 (2002)

12468722

Contact: Sessions A

Applied Trait Genetics

Syngenta Biotechnology Inc.

3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA

Email: allen.sessions@syngenta.com

ABRC Stock Number CS941192; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences.

Class: TDNA tagged.

Location/Qualifiers

FEATURES

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source
1..963
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/db_xref="taxon:3702"
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/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.6e-62;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 ACACCTGCTAAATTAATGAGTTCCTTTTCTTTGTTTTCAGCAAGTTACCTGTTACTTGAG 1246
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QY 1247 AGTTGAGTTAAATGGTAGTAAACGCAATTTAACCTTTATTAAGTTTAAATCGTATTCACAGAA 1306
DB 139 AGTTGAGTTAAATGGTAGTAAACGCAATTTAACCTTTATTAAGTTTAAATCGTATTCACAGAA 198

QY 1307 TCACCCAGAGACTTTAAATAAATCCATCGTAAACCTCCACTTCAAAATTCITTTAAAAA 1366
DB 199 TGACCCAGAGACTTTAAATAAATCCATCGTAAACCTCCACTTCAAAATTCITTTAAAAA 258

QY 1367 GTAGCAAAATCATTTAAATATTGTAAGTTTGTTCATTTCGAAATTTAGTACAGATCTCA 1426
DB 259 GTAGCAAAATCATTTAAATATTGTAAGTTTGTTCATTTCGAAATTTAGTACAGATCTCA 318

QY 1427 AAGCTCCTCTCTGTCGACATATCTCTCTTAACAAACGATAGTAACACTTGACCAACAGT 1486
DB 319 AAGCTCCTCTCTGTCGACATATCTCTCTTAACAAACGATAGTAACACTTGACCAACAGT 378

QY 1487 TTGACTTCTCGCGGGTTTCAT 1507
DB 379 TTGACTTCTCGCGGGTTTCAT 399

RESULT 4
BH846526
LOCUS SALK_008569.45.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_008569.45.50.x, genomic
survey sequence.
ACCESSION BH846526
VERSION BH846526.1 GI:21417397
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 328)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadranab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At3g02580.
Class: TDNA tagged.
Location/Qualifiers
1..700

source
1..328
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/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_008569.45.50.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 10.2%; Score 299.4; DB 9; Length 328;
Best Local Similarity 96.4%; Pred. No. 1.9e-57;
Matches 317; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 872 ATTCATGTCTCTCTCAACCTTTCCAAATTAATTTGTTTCAAAACATTTGCTCTCTAGTTT 931
DB 1 ATTCATGTCTCTCTCAACCTTTCCAAATTAATTTGTTTCAAAACATTTGCTCTCTAGTTT 60

QY 932 AAAACATGTAATGTTTGCATGATCTTTGCAAGACTCCATTTTGTGTTTAAGGTAACCTTG 991
DB 61 AAAACATGTAATGTTTGCATGATCTTTGCAAGACTCCATTTTGTGTTTAAGGTAACCTTG 120

QY 992 AATCTCATAGATTGTCGATTTGTTGTTATTTCCATTTTCAGGTACCGTCTCTAGACTGTA 1051
DB 121 AATCTCATAGATTGTCGATTTGTTGTTATTTCCATTTTCAGGTACCGTCTCTAGACTGTA 180

QY 1052 GTCTTGCTGACGAGTCGGCTTAACACCCCAAAATTTCAAAGATCTCACCAATCAAAATG 1111
DB 181 GTCTTGCTGACGAGTCGGCTTAACACCCCAAAATTTCAAAGATCTCACCAATCAAAATG 240

QY 1112 CTGGCTGGCCCCCAATATATAGATGGGCCAGTTAATCCGCTAGCTTTTACTCTTTAGACCT 1171
DB 241 CTGGCTGG-CCCAATATATAGATGGGCCAGTTAATCCGCTAGCTTTTACTCTTTAGACCT 299

QY 1172 ACCTTAGACAGTTAGACACACCTGCTAATTA 1200
DB 300 ACCTTAGACAGTTAGACACACCTGCTAATTA 328

RESULT 5
BH956101
LOCUS odg94b06.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BH956101
VERSION BH956101.1 GI:23437328
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 700)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg94 row: b column: 06
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
1..700

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/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pORW13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO100DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

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ORIGIN

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Query Match          9.8%; Score 285.6; DB 9; Length 700;
Best Local Similarity 83.0%; Pred. No. 3.1e-54;
Matches 365; Conservative 0; Mismatches 64; Indels 11; Gaps 3;

QY 2397 ATGTTTTCGGGTTTTCAGGGCTCGCATTCATCCCGTGGAGGGATCTTCAGGCTATA 2456
Db 52 AAGTTTTCGGGTTTTCAGGGCTCGCATTCATCCCGTGGAGGGATCTTCAGGCTATA 111
QY 2457 CGCAGCTGATAGCGCTGTTTATAGTGGCGATTCTCTCATACACATCTGAGTCTTTTG 2516
Db 112 CGCATGTGATAGCTGTTTATAGTGGCGATTCTCTCATACACATCTGAGTCTTTTG 171
QY 2517 TTTTTCGAGGGATATGGACAGCAAGCATCCATGTTGCATACATGTTGAACATCTGGCCT 2576
Db 172 ATTATGGAAGGGATATGGACAGCAAGCATCCATGTTGCATACATGTTGAACATCTGGCCT 231
QY 2577 ATAATGGGTGCGAGTACCATACATACACATACCAACATACCAAGCATAACTATGTCAT 2636
Db 232 ATAATGGGTGCGAGTACCATACATACCAACATACCAACATAACTATGTCAT 291
QY 2637 TATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2696
Db 292 TATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 351
QY 2697 AGTTTCAAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2748
Db 352 AGCTTTAATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 410
QY 2749 ATATGTTGCTCTTCTCGTGAATCTTATTAACATCTTCTTAATCAGTCTGGTGAATATA 2808
Db 411 ATGTTGTTTCTACTCTCTGAGTCTTA--AACCTTCTGAATATCAGTCTGTTAGATTAAGA 468
QY 2809 AACATGACTGCATAATTTGA 2828
Db 469 AACATGATGCACTATTAGA 488

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RESULT 6
CB255600          326 bp mRNA linear EST 31-DEC-2004
LOCUS
DEFINITION
36-E018428-019-008-G10-T7R MP1Z-ADIS-019 Arabidopsis thaliana cDNA
clone MP1Zp768G108Q 5-PRIME, mRNA sequence.
ACCESSION
CB255600
VERSION
CB255600.1 GI:56916225
KEYWORDS
EST.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 326)
REFERENCE
Jakoby,M., Stracke,R., Soerensen,T.R. and Weisshaar,B.
Arabidopsis thaliana cDNA library enriched in transcription factors
Unpublished (2003)
AUTHORS
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de

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Insert Length: 326 Std Error: 0.00
Plate: 8 row: G column: 10
Seq primer: T7R; CTAATAGACTCACTATAGGGA.
Location/Qualifiers
1..326
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/cultivar="At7"
/db_xref="GABI:596808"
/db_xref="taxon:3702"
/clone="MP1Zp768G108Q"
/tissue_type="hypocotyl"
/dev stage="tissue culture"
/lab_host="E. coli DH5alpha mcr"
/clone_lib="MP1Z-ADIS-019"
/notes="Vector: pSPORI1; Site 1: NotI primer adapter;
Site 2: SalI primer adapter; RNA from cellucyte (At7) 5
days after inoculation treated with 0.002 mM cycloheximid
for 2 h in the dark. Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de. This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

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ORIGIN

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Query Match          9.7%; Score 284.4; DB 6; Length 326;
Best Local Similarity 97.7%; Pred. No. 5.2e-54;
Matches 299; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 697 TGGATGATTTGGATTTGGCTCTCTTAGGGATTCCTCTTAGAAGAAGATGACACAAA 756
Db 9 TGGGTGATTTGGATTTGGCTCTCTTAGGGATTCCTCTTAGAAGAAGATGAC-ACAAA 67
QY 757 GACAGCTTCAAGAAAGAGAGTGAGATGCCACCTTGGTGTCTTCTCTCTCTTCTCT 816
Db 68 GACAGCTTCAAGAAAGAGAGTGAGATGCCACCTTGGTGTCTTCTCTCTCTTCTCT 127
QY 817 TGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 876
Db 128 TGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 187
QY 877 TGTGTCTCTCTCAACCTTTCATATATATGTTTACAAATTTGCTGTCTAGTTTAAAC 936
Db 188 TGTGTCTCTCTCAACCTTTCATATATATGTTTACAAATTTGCTGTCTAGTTTAAAC 247
QY 937 ATGTAATGTTTGTGATGATCTTTGCAAGACTCCATTTTCTTAAAGTAAACCTTGAATCT 996
Db 248 ATGTAATGTTTGTGATGATCTTTGCAAGACTCCATTTTCTTAAAGTAAACCTTGAATCT 307
QY 997 CATAGA 1002
Db 308 CATAAA 313

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RESULT 7
CL488421
LOCUS
DEFINITION
SAIL 508_H08.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_508_H08.v1, genomic survey sequence.
ACCESSION
CL488421
VERSION
CL488421.1 GI:45969313
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1016)
REFERENCE
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmery,B.,
Mittel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)

```


Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g02580.
 Class: TDNA tagged.

FEATURES

source
 1. .327

Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /scot_type="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_136266.46.25.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 9.5%; Score 278.4; DB 9; Length 327;
 Best Local Similarity 99.6%; Pred. No. 1.2e-52; Indels 0; Gaps 0;
 Matches 279; Conservative 0; Mismatches 1;
 QY 1 GTTTGGTATTATTGGATGCACAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT 60
 DB 280 GTTTGGTATTATTGGATGCACAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT 221
 QY 61 CCATGCCACCATCATATCTACAAAGCAGATACACTCTCTCCATTTGCCGGTAAGTG 120
 DB 220 CCATGCCACCATCATATTTACAAAGCAGATACACTCTCTCCATTTGCCGGTAAGTG 161
 QY 121 TTTTCAGTTTGTCTCTTTAGTTCTTTGTAAGAGTTGTTAGTATTTCTTACCAG 180
 DB 160 TTTTCAGTTTGTCTCTTTAGTTCTTTGTAAGAGTTGTTAGTATTTCTTACCAG 101
 QY 181 AAAAGACTTTGTGACAGCTGCTTGTAACCAATCACAATTTTGCAATTCCTTATCCATAA 240
 DB 100 AAAAGACTTTGTGACAGCTGCTTGTAACCAATCACAATTTTGCAATTCCTTATCCATAA 41
 QY 241 AGTAACCAAGAGGCTAGAAATTAATATATATGTCAGCTGCA 280
 DB 40 AGTAACCAAGAGGCTAGAAATTAATATATATGTCAGCTGCA 1

RESULT 10

CD823327
 LOCUS BN25.048G14F020110 BN25 Brassica napus cDNA clone BN25048G14, mRNA
 DEFINITION sequence.
 ACCESSION CD823327
 VERSION CD823327.1 GI:32505267
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 482)
 REFERENCE
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)

COMMENT

Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES

source
 1. .482
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
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 /db_xref="taxon:3708"
 /clone="BN25048G14"
 /tissue_type="seed"
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ORIGIN

Query Match 9.1%; Score 265.4; DB 6; Length 482;
 Best Local Similarity 84.5%; Pred. No. 1.2e-49; Indels 1; Gaps 1;
 Matches 310; Conservative 0; Mismatches 56;
 QY 462 TTTACAGGCTTGCATTCACCCAGTAGCGGATCTTAAGCTGTACCGCATGTGATAG 521
 DB 29 TTGCCGGGCTTGCGTTTCACCCAGTAGATGGATTCTTCAGGCTTTACCGCATGTGATAG 88
 QY 522 CGCTG-TTATAGTGCATTCATTTTCACAACTCATATAGTCTTTGTTTCATGGAAGCGA 580
 DB 89 CTCTCTTTATAGTGCATTCATTTTCACAACTCATATAGTCTTTGTTTCATGGAAGCGA 148
 QY 581 TATGACGCGGAACATCCATGACTGCATCCATGCAGCAACATCTGGCCAGTAATGGGTGCAG 640
 DB 149 TATGACGCGGAACATCCATGACTGCATCCATGCAGCAACATCTGGCCAGTAATGGGTGCAG 208
 QY 641 GATACCATACATACACCAACGACATCAAGCAATCAATGCTCATTTATACATATGA 700
 DB 209 GGTACCATACATACACCAACGACATCAAGCAACATCAATGCTCATTTATACATATGA 268
 QY 701 TGGATTGATGTTGGCTCTCTTAGGGATCCCTCTTAGAAGAGATGACACAAAGACA 760
 DB 269 TGGATTGATGTTGGCTCTCTTTAAAGACCCCTCTTTTAAAGATGTTGACAAAGACA 328
 QY 761 GCTTCAAGAAAGACAGAGTGAAGATGCCCACTTGGGTTTTGTTCTCTCTTTGTTGTGTG 820
 DB 329 TCTCCAGAAAGACAGAGTGAAGATGCCCTTTGTTGTTGTTGTTCTTCTTCTTCTTCTT 388
 QY 821 TTGTTGT 827
 DB 389 TTACTTT 395

RESULT 11

CD834242
 LOCUS BN45.041B07F011207 BN45 Brassica napus cDNA clone BN45041B07, mRNA
 DEFINITION sequence.
 ACCESSION CD834242
 VERSION CD834242.1 GI:32516182
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 644)
 REFERENCE
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.inbiohogen.fr>.

FEATURES

source
1. .644
Location/Qualifiers
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/db_xref="taxon:3708"
/clone="BN45041B07"
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ORIGIN

Query Match 8.5%; Score 249.8; DB 6; Length 644;
Best Local Similarity 88.0%; Pred. No. 4.8e-46;
Matches 272; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 2022 AGAATCCATCTCCAGAGAAAGCAATGCTTTGGCAATATACGTCGCAATGAAGGCTAT 2081
Db |||||
QY 236 AGATTCTATTCTTACAGAAAGCAATGATTGAGCAATATACATGTGGCAGTGAAGGAT 295
Db |||||
QY 2082 GCCTGGTACATCTCTCCAGCTCTCTGAGTATATATGAGCATGCTTGGACCAA 2141
Db |||||
QY 296 GCCTGGTATACACTTTTCCCAACTCTCTGAGTATATATGAGCATGCTTGGACCAA 355
Db |||||
QY 2142 ATGTACTCTACACTTGACATTTCAACTGTTCTCTGTTCTCTACATAGCTCTCTA 2201
Db |||||
QY 356 ATGTACTCTACACTTGACATTTCAACTGTTCTCTGTTCTCTACATAGCTCTCTA 415
Db |||||
QY 2202 TCTGTTTATGAGTATGATTTATGTTGGTTTCAAGAGCTTTCATGACATTAAT 2261
Db |||||
QY 416 TCTCTTATGATGAGTTGGTATGATTTGTTTCAAGAGCTTTCATGACATTAAT 475
Db |||||
QY 2262 TCTCTATAGCATCTCCAGCTTACCATCATATATGATACACAGCAAAACACATCTCTCC 2321
Db |||||
QY 476 TCTCTATAGCATCTCTCCAGCTTACCATCATATGATACACAGCAAAACACATCTCTCC 535
Db |||||
QY 2322 ATTTGCCGG 2330
Db |||||
QY 536 ATTTGCTGG 544
Db |||||

RESULT 12

CK264500/c
LOCUS
DEFINITION
EST710578 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAB706 3' end, mRNA sequence.

ACCESSION

CK264500
CK264500.1 GI:39821478
EST.
Solanum tuberosum (potato)

SOURCE

Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE

Buell, C.R., Hart, A., Zimmann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST710577

AUTHORS

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org

TITLE

Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>

COMMENT

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
1. .869
/organism="Solanum tuberosum"
/mol_type="mRNA"

FEATURES

source

/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB706"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH108-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site: 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

Query Match 7.8%; Score 228.4; DB 7; Length 869;
Best Local Similarity 62.7%; Pred. No. 3.9e-41;
Matches 424; Conservative 0; Mismatches 166; Indels 86; Gaps 1;
QY 2022 AGAATCCATCTCCAGAGAAAGCAATGCTTTGGCAATATACGTCGCAATGAAGGCTAT 2081
Db |||||
QY 789 AGATGCCATACCATCAAGAGCAATGCTCTTGGCAATATACGTTGCTATGAAGCTAT 730
Db |||||
QY 2082 GCCTGGTACATCTCTTCCAGCTGTCTCTGAGTATATATGAGCATGCTTGGACCAA 2141
Db |||||
QY 729 GCCGTGGTACTGTGCCCTTCCATCACTTCTGAAATACATGATGAACGGATGGACCAA 670
Db |||||
QY 2142 ATGTACTCTACACTTGACATTTCAACTGTTCTCTGTTCTCTCTATAGCTCTCTA 2201
Db |||||
QY 669 ATGTTTTCGAGAAATAGTATGTTGGATGGCTACCTACATCATCAATCGGCTATT 610
QY 2202 TCTGTTTATGATGATTTATGATTTATGTTGGTTTCAAGAGCTTTCATGACATTAAT 2261
Db |||||
QY 609 TCTTGAATAGTGGAGTTTGAATCTACTGATGCAAGTTGTTGTCATGACATAAACC 550
QY 2262 TCTCTATAGCATCTCCAGCTTACCATCATATGATACACAGCAAAACACATCTCTCC 2321
Db |||||
QY 549 TCTGACAAATATCTGCAATGATACATATTTTACAAACAGCAAAACACACTTTTCCC 490
QY 2322 ATTTGCCGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
Db |||||
QY 489 GTTGTCTGATG-----GCATTCACCCATGGATGGA 456
QY 2382 TGACTTCTTTACTTGATGTTTTCGGGTTTTCAGGGCTGCGATTCATCCGCTGGACGGG 2441
Db |||||
QY 476 -----GCATTCACCCATGGATGGA 456
QY 2442 ATACTTACGGCTATACCCGACGTGATAGGCTGTTTATAGTCCCATTCATCTCAATACA 2501
Db |||||
QY 455 ATACTGACGGCAGTCCACACGTTGCTCTTATTTCTTGGTGCCCAATGCAATTTCACTACA 396
QY 2502 CATCTGAGCTCTTTGTTTGGAGGGGATATGAGCAGCAAGCATCCATGATGCAATACAT 2561
Db |||||
QY 395 CACATAGCACTCATATTTCTTGAAGCCTTATGAGCAGCTATATTTTCACTGACTGCATACAT 336
QY 2562 GGTAACATCTGGCCTTATATGGTGGCAGGATACCATACCATACACATACAAACATAAAG 2621
Db |||||

Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

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Location/Qualifiers
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/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POABT06"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 7.8%; Score 227; DB 7; Length 924;
Best Local Similarity 62.7%; Pred. No. 8.3e-41;
Matches 422; Conservative 0; Mismatches 165; Indels 86; Gaps 1;

QY 2022 AGAATCCATCTTACGAGAAAGCAATGCTTTTGGCAAATATACGTGGCAATCAAGCTAT 2081
DB AGATGCCATACCATCAAGAGCAATGCTCTTGCAAATATCAGTTGCTATGAAGCTAT 397
QY 2082 GCCTTGGTACATCTCTTCCAGCTCTCTGAGTATATGATCGAGCATGGTTGACCAA 2141
DB GCGTGGTACTGTGCGCTTCCATCACTTTCTGAATACATGATGAAACGGATGGACCAA 457
QY 2142 ATGTTACTCTACACTTGACATTTCAACTGGTTCTCTGTTCTCTCTACATAGCTCTCTA 2201
DB ATGTTTTCGAGATTAAGTATGTTGGATGGCTCTACCTACATCATCATGCGCTATTTA 517
QY 2202 TCTTGTTTTATGTTAGTTATGATTTATTTGGTTTCAAAAGAGCTTCATGACATTAAT 2261
DB TCTTGTAAATAGTGGAGTTTGGAACTCTACTGGATGCAAAAGTTGTCATGACATAAACC 577
QY 2262 TCTCTATAGCATCTCCATCGCTACCCATCATATGATACACAGCAAAACAGCTCTCTCC 2321
DB TCTGTACAAATATCTGCTGCTACATCATATTTTACAAACAGCAAAACAGCTTTCCCC 637
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DB GTTTGCTGATTTG----- 650
QY 2382 TGACTTCTTTTATCTGATGTTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGACGGG 2441
DB -----GCATTCACCCATTTGGATGGA 671
QY 2442 ATACTTCAGCTATACCGCAGTATAGCGCTGTTTATAGTCCGATTCATCTCATACA 2501
DB ATACTGCGGAGTGCACACCGTTGTAGCTCTATTCTTGTGTCCTCAATGCTATTTCTACA 731

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QY 2502 CATCTGAGTCTTTTGTGTTGGAAGGATATGACAGCAAGCATCCATGATTGCATACAT 2561
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QY 2562 GGTAACATCTGCGCTATATATGAGTGCAGGATACCATACATACACCATACATACAG 2621
DB GGTAAGGTGTGCGCTGTAAATGGGTGCGGCTATATACATTCACCATACATACACCGC 851
QY 2622 CATACTATGTCATTATACCATATGAGTGGACTGATGTTGGCTCTCTTATGTTCTCT 2681
DB CATAATTTATGTCATTATACATATGAGTGGACTGATGTTGGAACTCTACGTATCTCC 911
QY 2682 TTAGCAGAAAAG 2694
DB GTTGAAGAGGATG 924

RESULT 15
CN731853
LOCUS
DEFINITION
24RDBNH UP 023 G12.12JAN2004.084 Brassica napus 24RDBNH Brassica
napus cDNA 5', mRNA sequence.
ACCESSION
CN731853
VERSION
CN731853.1 GI:65289668
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 753)
AUTHORS
Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.
TITLE
Gene Expression Patterns during Brassica Zygotic Embryogenesis
JOURNAL
Unpublished (2004)
COMMENT
Contact: Raju Datla
Molecular and Developmental Genetics
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 5267
Fax: 306 975 4839
Email: Raju.Datla@nrc-cnrc.gc.ca
High quality sequence stop: 753.
FEATURES
Location/Qualifiers
1..753
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 24RDBNH"
/note="Vector: pDNR-LIB CREATOR; Site 1: Sfi I A; Site 2:
Sfi I B; Zygotic embryos at heart stage from Brassica
napus seeds were used for the isolation of PolyA RNA and
in the construction of the cDNA library. Sequences have
been trimmed to remove vector and low quality regions
using LUCY sequence cleanup software (www.tigr.org)."

ORIGIN

Query Match 7.7%; Score 226.6; DB 7; Length 753;
Best Local Similarity 69.2%; Pred. No. 9.9e-41;
Matches 370; Conservative 0; Mismatches 79; Indels 86; Gaps 1;

QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGGCAAATATACGTGGCAATCAAGCTAT 2081
DB AGATGCTATTTCGACAGAAAGGCTATGCTTTTGGCAATCTATGTCGCAATGAGCGAT 364
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DB GCCTTGGTACACTCTGCTTCCAACTGTATCTGAGTATATGATGAAAGTGGATGACTAA 424
QY 2142 ATGTTACTCTACACTTGGACCATTTCAACTGGTTCTCTGTTCTCTCTACATAGCTCTCTA 2201
DB ATGTTACTCGAGAGTAGCGAAGTCAAGTCAAGCTGCTCTCTACTTTGTTTCAATCGGACATA 484

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Qy 2202 TCTTGTGTTTGTAGTTGAGTTTATGATTTATTGGGTTTCAAAAGAGCTTTCATGACATTTAAATT 2261
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Qy 485 TCTGTGTTTGTAGTCGAGTTTGGTATTTATTGGATGCAAGAGCTTTCATGACATTTAAGCC 544
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAGCAAAACACACTCTCTCC 2321
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 545 TCTCTATAAGTATCTCCATGCCACCCATCATATCTACAACAAACAGATACACTCTCTCC 604
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2322 ATTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGG 2381
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 605 CTTTGGC----- 611
Qy 2382 TGACTTCTTTTACTTGTATGTTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGG 2441
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 612 -----GGGCTTGGGTTTCACCCACTAGACGGG 638
Qy 2442 ATACTTCAGGCTATACCGACGCTGATAGCGCTGTTTTATAGTCCGATTCATCTCATPAACA 2501
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Qy 639 ATACTTCAAGCTGTACCGCACGTTGTTGCTTTTATAGTCCGATTCATTTCAACAACC 698
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Qy 2502 CATCTGAGTCTTTTGTGTTTGGAGGGATATGGACAGCAAGCATCCATGATTGCA 2556
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Qy 699 CATCTAGTCTTTTGTGTTTATGGAAGCGATATGGACAGCAAGCATCCATGACTGCA 753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: March 7, 2006, 12:18:47
Job time : 11155 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:11:04 ; Search time 504 Seconds
(without alignments)
10316.206 Million cell updates/sec

Title: US-10-736-318-22
Perfect score: 2925
Sequence: 1 gtttggtatttattggtgc.....tcaatttgactaatctg 2925

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	15.8	1175	3	US-09-885-723-23
2	203.4	7.0	1447	3	US-09-443-041A-27
3	188	6.4	1210	3	US-09-443-041A-29
4	187	6.4	911	3	US-09-443-041A-23
5	179.6	6.1	1318	3	US-09-443-041A-25
6	173.8	5.9	1070	3	US-09-443-041A-9
7	118.4	4.0	300	3	US-09-313-294A-4514
8	90.8	3.1	269	3	US-09-313-294A-379
9	90	3.1	459	3	US-09-443-041A-13
10	82.8	2.8	314	3	US-09-313-294A-7458
11	77.8	2.7	7218	2	US-08-232-463-14
12	71	2.4	495	3	US-09-443-041A-15
13	69.4	2.4	360	3	US-09-443-041A-11
C 14	68	2.3	612	3	US-09-902-540-1357
C 15	60.6	2.1	614	3	US-09-902-540-1318
C 16	60.6	2.1	1141	3	US-09-806-708B-22
C 17	59.6	2.0	1039	3	US-09-902-540-1280
18	56.8	1.9	2039	3	US-09-949-016-2275
19	56.8	1.9	2092	3	US-09-949-016-901
20	56.2	1.9	396	3	US-09-640-173-53
21	56.2	1.9	396	3	US-09-713-550-53
22	56.2	1.9	396	3	US-09-825-294-53
23	56.2	1.9	396	3	US-09-970-966-53
C 24	55.2	1.9	19124	2	US-08-487-826B-13

C 25	53.8	1.8	240	2	US-08-628-417-6	Sequence 6, Appli
C 26	53.2	1.8	1141	3	US-09-806-708B-22	Sequence 22, Appl
C 27	52.8	1.8	4167	3	US-09-973-278-700	Sequence 700, App
28	52.8	1.8	9277	3	US-09-949-016-14017	Sequence 14017, A
29	52.8	1.8	21168	3	US-09-949-016-12643	Sequence 12643, A
C 30	51.4	1.8	2447	2	US-09-014-969-14	Sequence 14, Appl
C 31	51.2	1.8	1098	3	US-09-614-221A-113	Sequence 113, App
C 32	50.8	1.7	1696	3	US-08-835-811-1	Sequence 1, Appli
C 33	50.2	1.7	658	3	US-08-998-416-595	Sequence 595, App
C 34	49.4	1.7	41736	3	US-09-949-016-17091	Sequence 17091, A
C 35	49	1.7	282	3	US-09-621-976-18648	Sequence 18648, A
C 36	48.8	1.7	832	3	US-09-621-976-2813	Sequence 2813, Ap
C 37	48.6	1.7	5852	2	US-07-867-106-2	Sequence 2, Appli
C 38	48.2	1.6	145241	3	US-09-949-016-17394	Sequence 17394, A
C 39	48.2	1.6	145241	3	US-09-949-016-17395	Sequence 17395, A
C 40	48	1.6	237510	3	US-09-949-016-14273	Sequence 14273, A
C 41	47.8	1.6	1662	3	US-09-668-097A-13	Sequence 13, Appl
C 42	47.8	1.6	50000	3	US-09-662-254B-25	Sequence 25, Appl
C 43	47.8	1.6	54033	3	US-09-949-016-12091	Sequence 12091, A
C 44	47.8	1.6	54033	3	US-09-949-016-14325	Sequence 14325, A
C 45	47.6	1.6	603	3	US-09-248-796A-5211	Sequence 5211, Ap

ALIGNMENTS

RESULT 1

US-09-885-723-23
; Sequence 23, Application US/09885723
; Patent No. 6822142

GENERAL INFORMATION:

; APPLICANT: Monsanto Company
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS
; FILE REFERENCE: MTC6783.1
; CURRENT APPLICATION NUMBER: US/09/885,723
; CURRENT FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-885-723-23

Query Match 15.8%; Score 461; DB 3; Length 1175;
Best Local Similarity 97.6%; Pred. No. 3e-108;
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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QY	521	GGGCTG-TTATAGTGCCAAATTCATTTCACACTCATATAGGCTCTTTGTTTCATGGAAGG	579
Db	703	GGCTGTTTATAGTGCCAAATTCATTTCACACTCATATAGGCTCTTTGTTTCATGGAAGG	762
QY	580	ATATGGACGGCGAAACATCCATGACTGTCATCCATGGCAACATCTGCCAGTATATGGGTGCA	639
Db	763	ATATGGCGGGGCAACATCCATGACTGTCATCCATGGCAACATCTGCCAGTATATGGGTGCA	822
QY	640	GGATACCATACGATACACACACGACATACCAAGCAATACTATGGTCAATATACCATATGG	699
Db	823	GGATACCATACGATACACACACGACATACCAAGCAATACTATGGTCAATATACCATATGG	882
QY	700	ATGATGTTGGATGTTGGCTCTCTTTAGGATCCTCTCTTAGAGAGAGATGACAAACAGAC	759
Db	883	ATGATGTTGGATGTTGGCTCTCTCTTTAGGATCCTCTCTTAGAGAGAGATGACAAACAGAC	942
QY	760	AGCTTCAAGAAGCAGAGTGAGAAATGCCCACTTGGGTTTGTCTTCTTCTTTGTTCTTGT	819
Db	943	AGCTTCAAGAAGCAGAGTGAGAAATGCCCACTTGGGTTTGTCTTCTTCTTCTTGTCTTGT	1002
QY	820	GTTGTTGTTGTTCAAAAGTTTCAGCCTTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT	879

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Db 1063 GTCTCTCTCAACCTTTCCAAATATATGTTACAAACATTTGCTGTCTAGTTTAAACATG 1122
Qy 940 TAAATGTTTGTGATGATCTTTGCC 960
Db 1123 TAAATGTTTGTGATGATCTTTCC 1143

RESULT 2

US-09-443-041A-27
; Sequence 27, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 1447
; TYPE: DNA
; ORGANISM: Glycine max
US-09-443-041A-27

Query Match 7.0%; Score 203.4; DB 3; Length 1447;
Best Local Similarity 61.3%; Pred. No. 5e-42;
Matches 399; Conservative 0; Mismatches 166; Indels 86; Gaps 1;
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Qy 2142 ATGTTACTCTACACTTGGACCATTTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTA 2201
Db 436 GTGCTATCTAGATTATATAATGTTGGTTGGCTTGCATACCTTGTGTATTAGCAATTTA 495
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Qy 2262 TCTCTATAGCATCTCCATGCTACCCATCATATGTACAAACAGCAAAACACACTCTCTCC 2321
Db 556 GCTTTTCAAAATATCTTCTGCTACCTACCATCATCTCTAATAACAGAACACTCTCTCCC 615
Qy 2322 ATTTGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
Db 616 TTTTGTGGTTG----- 628
Qy 2382 TGACTTCTTTACTGTGATGTTTTCGGGTTTTCAGGCTCGCATTCATCCGCTGGACGGG 2441
Db 629 -----GCATTTCAACCCTCTTGATGGG 649
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Db 650 ATACTTCAGGCTATACCGCATAGCCCTTGTGTTGTTTTTATGCGCAATTCATTTACTCA 709
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Db 710 CATTTGGCCCTCATATTCAATTCAGGGCGTTGGACTGCAAAATATTTCATGATTGCATTCAT 769
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Db 770 GGAATAATTGTGGCCTGTTATGGGTGCTGTTTACCAACACATTCATCACATACATATCGG 829
Qy 2622 CATAACTATGTCATTATACCATATGGATGGATGGACTGGATGTTTGGCTCTCTT 2672
Db 830 CACAACCTAGCCCACTACACCATATGGATGGATGGATGGATGGATGGATGGATGGAT 880

RESULT 3

US-09-443-041A-29
; Sequence 29, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1129
; OTHER INFORMATION: any nucleotide
US-09-443-041A-29

Query Match 6.4%; Score 188; DB 3; Length 1210;
Best Local Similarity 59.8%; Pred. No. 4.2e-38;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;
Qy 2022 AGAATCCATTCCTACGAGAAAGCAATGCTTTTGCAAATATATACGTCGGAATGAAGCTAT 2081
Db 188 AGATGCTCTCCCTACAGTAGAAGCTATGAAGAAGCAATAATTTGTCATCAAGGCTAT 247
Qy 2082 GCCTGGTACACTCTTCTCCAGCTGCTCTGAGTATATGATCGACATGGTTGGACCAA 2141
Db 248 GCCTTTCTACTGTGCTCTTCCGTCGCTATCTGAGCACATGATTTGAGAGTGGATGGACAG 307
Qy 2142 ATGTTACTCTACACTTGGACCATTTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTA 2201
Db 308 GTGTTTCTTTCATATCAGCGAAGTTGGTTGGCTATATGATATATCTATGTCTCTATA 367
Qy 2202 TCTCTGTTTGTAGTTTATGATTTATTTGGTTTTCACAAAGAGCTTCATGACATTAAT 2261
Db 368 TCTCATCTTTGTGGAGTTCCGGAATTTACTGGATGACAGAGAGTTGTCATGACATAAGCC 427
Qy 2262 TCTCTATAGCATCTCCATGCTACCCATCATATGTAACAAAGCAAAACACACTCTCTCC 2321
Db 428 ACTATACAAGCACCTTACATGCAACCCACCAACATTTTACAACAGGAGAAATACCCATACCC 487
Qy 2322 ATTTGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
Db 488 ATTTG----- 492
Qy 2382 TGACTTCTTTACTGTGATGTTTTCGGGTTTTCAGGCTCGCATTCATTCGCTGGACGGG 2441
Db 493 -----CTGACTAGCATTCATCCATTCATGGACGGG 521
Qy 2442 ATACTTCAGGCTATACCGCAGCTGATAGGCTGTTTATAGTCGGATTCATCTCATACA 2501
Db 522 ATACTGCAAGCCATATCGCAGCTGATGCTGTTCTCTTCTCCGATGCACTTTCAGGACG 581

QY 2502 CATCTGAGTCTTTTGGTGGGATATGACAGCAAGCATCCATGATTGCATACAT 2561
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Db 582 CACATTTGCTCTCTTATCATAGGCGGTGGAGCGCAAAATCCACGACTGCATCCAC 641
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QY 2562 GGTAAATCTGGCCTATATAGGTGAGGATACCATACATACACCATACATACAG 2621
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Db 642 GCGAAGATCTGGCGGTGATGGCGCGCGCTACCAACCATCCACACACGACGTACCG 701
|||
QY 2622 CATACTATGTCATTATACCATATATGATGGAGTGGATGTTTGGCTCTCT 2671
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Db 702 CACAATATGGCCACTACACCGTGGATGGAGTGGCTGTTTGGACCCCT 751
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RESULT 4
US-09-443-041A-23
; Sequence 23, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 911
; TYPE: DNA
; ORGANISM: Zea mays
US-09-443-041A-23

Query Match 6.4%; Score 187; DB 3; Length 911;
Best Local Similarity 59.8%; Pred. No. 6.7e-38;
Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps 1;
QY 2023 GAATCCATTCTTACGAGAAAGCAATGCTTTTGGAAATATACGTGGCAATGAAGGCTATG 2082
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Db 74 GATGCCATCCCCACAAATGAAGCTATGAAGAGCAAAATAGCTGTAGCATCCCAAGGCTATG 133
|||
QY 2083 CCTTGGTACACTCTTCTCCAGCTCTCTCTGAGTATATGATCGAGCATGTTGGACCAAA 2142
|||
Db 134 CCTTTTACTGTGCTCTTCCAACTTTATCTGAGTATATGATCGAGAGTGGATGGACCCGG 193
|||
QY 2143 TGTACTCTACACTTGACCATTTCAACTGGTTCCCTCTCTCTCTACATAGCTCTCTAT 2202
|||
Db 194 TGTACTTTAATATCAGCGAATGGTCTTCTGCAATACCTTTGTTATATGCTATGTAT 253
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QY 2203 CTGTTTGTAGTTGAGTTTATGATTTATGGGTTTCAAAAGAGCTTCATGACATTAATTT 2262
|||
Db 254 CTCAATTTTGTGGAGTTTGGAAATTTACTGGATGCAAGAGAGTTGATGACATAAAGCCA 313
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QY 2263 CTCTATAGCATCTCCATCTACCATCCATATATGATACAAAGCAAAACACACTCTCTCA 2322
|||
Db 314 CTATACAAACATCTGATCGACCCACCACCATATTTACAAAGGAGAACACCTTGTCTCG 373
|||
QY 2323 TTTGCGGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGATCAATGGT 2382
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Db 374 TTTGC----- 378
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QY 2383 GACTTCTTTACTGTATGTTTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGA 2442
|||
Db 379 -----TGGACTCGGTTTTCACCCACTGGATGTA 407
|||
QY 2443 TACTTCAGGCTATACCGACGTGATAGCGCTGTTTATAGTCCGATTCATCTCATACAC 2502
|||
Db 408 TTTCTGAACGATACCGCATGCTGTGGCTCTTCTCTCTCCCAAGCACTTCAGGACGC 467
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QY 2503 ATCTGAGTCTTTTGGTGGGATATGACAGCAAGCATCCATGATTGCATACATG 2562
|||
Db 468 ACATCGCTCTCGTGTCTTGGAGGCGGTGGAGCAAAATCCACGACTGCATTCACG 527
|||
QY 2563 GTAACATCTGGCCTATATAGGTGAGGATACCATACCATACCATACATACATACAG 2622
|||
Db 528 GCAAGTATGGCCAGTCATGGCGCTGGGTATCACACCATCCACCATACGACTTACCGCC 587
|||
QY 2623 ATAACTATGTCATTATACCATATATGATGGAGTGGATGTTTGGCTCTCT 2671
|||
Db 588 ACNACTATGGCCACTACACCGCTCTGGATGGAGTGGATGTTTGGTAGCT 636
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RESULT 5
US-09-443-041A-25
; Sequence 25, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-443-041A-25

Query Match 6.1%; Score 179.6; DB 3; Length 1318;
Best Local Similarity 58.6%; Pred. No. 6.3e-36;
Matches 389; Conservative 0; Mismatches 189; Indels 86; Gaps 1;
QY 2022 AGAATCCATTCTTACGAGAAAGCAATGCTTTTGGAAATATACGTGGCAATGAAGGCTAT 2081
|||
Db 351 AGATTCTATACCTACAAATCGAAGCTATGAAGAAGCAAAATATTTGTTCATCAAGGCTAT 410
|||
QY 2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGTTGGACCAA 2141
|||
Db 411 GCCTCTCTATTTGGCCCTTCCACCTTATCTGAGTACATGTTGAGATGGATGACACA 470
|||
QY 2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCTCTCTCTCTACATAGCTCTCTA 2201
|||
Db 471 GTGTTATGTTAATATCAGTGAAGTTGGTTGGCCAAATGTACCTGGTTTATCTGGCTTATA 530
|||
QY 2202 TCTTGTGTTAGTTTATGATTTTATGGTTTCAAAAGAGCTTCATGACATTAATTT 2261
|||
Db 531 TCTTATCTTGTGAGTTTGGAAATTTACTGGATGCAAGAGAGTTGCAATGACATAAAGCC 590
|||
QY 2262 TCTCTATAAGCATCTCCATGCTTACCATCATATGATACAAAGCAAAACACACTCTCTCC 2321
|||
Db 591 ATTGTCAAGTACCTTGACACATACCATCATTTTACAAAGGAGATACCTCATACACC 650
|||
QY 2322 ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGATCAATGG 2381
|||
Db 651 ATTTG----- 655
|||
QY 2382 TGACTTCTTACTGTATGTTTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGG 2441
|||
Db 656 -----CAGGACTAGCATTCATTCACCTGGATGGG 684
|||
QY 2442 ATACTTCAGGCTATACCGACGTGATAGCGCTGTTTATAGTCCGATTCATCTCATACAA 2501
|||
Db 685 ATTTTGAAGCCATACCGCATGTTTGGCTCTTACCTTATCCCAACACACTTCAGGACA 744
|||
QY 2502 CATCTGAGTCTTTTGGTGGAGGATATGACAGCAAGCATCCATGATTGCATACAT 2561
|||

Db 745 CACATTGCTCTCTTTGTCATAGAGCGGTGTGGAGCACTTAACTCAATCCATGACTGCATTAC 804
QY 2562 GGTAAACATCGGCCTATAATAGGTGAGGATACCATACCATACCAATCAACATACAAG 2621
Db 805 GCGAAGTTTGGCCGGTCTATGGGTGCTGGCTATCACCAATTCACCATACCAATACACCGT 864
QY 2622 CATACATATGGTCATTTATACCATATGAGTGGAGTGGATGCTTTGGCTCTTATGGTTCT 2681
Db 865 CACAACATATGGCCACTACACCGGTGTGGAGTGGATGCTTGGCCACCCCTTCGAGAGCCA 924
QY 2682 TTAG 2685
Db 925 GAAG 928

RESULT 6

US-09-443-041A-9
; Sequence 9, Application US/09443041A
; Patent No. 645717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafaleki, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; PRIOR FILING DATE: 1999-11-18
; CURRENT APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1070
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure (886)
; LOCATION: (885)
; OTHER INFORMATION: any nucleotide
; NAME/KEY: unsure
; LOCATION: (949)
; OTHER INFORMATION: any nucleotide
; NAME/KEY: unsure
; LOCATION: (1019)
; OTHER INFORMATION: any nucleotide
; NAME/KEY: unsure
; LOCATION: (1050)..
; OTHER INFORMATION: any nucleotide
; NAME/KEY: unsure
; LOCATION: (1058)
; OTHER INFORMATION: any nucleotide

US-09-443-041A-9

Query Match 5.9%; Score 173.8; DB 3; Length 1070;
Best Local Similarity 58.3%; Pred. No. 1.8e-34;
Matches 379; Conservative 0; Mismatches 185; Indels 86; Gaps 1;
QY 2022 AGAATCCATTCTTACGAGAAAGCAATGCTTTTGCAGATATAGCTGGCAATGAAGGCTAT 2081
Db 395 AGATGCCATCCCAAAATGAAGCTATGAGAAGCAATAGCTGTAGCATCCAAAGCTAT 454
QY 2082 GCCTTGGTACACTCTTCTCCAGCTGTCTGTAGTATATGATCGAGCATGGTTGGACCA 2141
Db 455 GCCTTTTACTGTGCTCTTCCAACTTTATCTGAGTATATGATCGAGAGTGGATGGACCG 514
QY 2142 ATGTTACTCTACACTTGAACATTTCAACTGGTTCCTCTGTTCTCTACATAGCTCTCTA 2201
Db 515 GTGTTACTTTTAAATACAGCGAAATGGGTTTTCTGCAATACCTTTGTTATATGGCTATGTA 574
QY 2202 TCTTGTGTTTGTAGTTGAGTTTATGATTTTATGGGTTTCAAGAGCTTCATGACATTAAT 2261

Db 575 TCTCATTTTTTGTGGAGTTTGGAAATTTACTGGATGCACAGAGAGTTGTCATGACATAAGCC 634
QY 2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACACAGCAAAACACACACTCTCTCC 2321
Db 635 ACTATACAAACATCTGCATGCGACCCCATATTTTACAAAGGAGAACACCTTGTCTCC 694
QY 2322 ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATTTAAATTCAAGAGCTTGTATCAATGG 2381
Db 695 GTTTG----- 699
QY 2382 TGACTTCTTTTACTTGATGTTTTTCGGGTTTTTCAGGCTCGCATTTCCATCCGCTGGACGG 2441
Db 700 -----CTGGACTCGCGTTTTTACCACCTGGATGGT 728
QY 2442 ATACTTCAGGCTATACCGCATGATAGCGCTTTTATATAGTCCGATTCATCTCATAAACA 2501
Db 729 ATTCTGCAAGCATATCCGCATGTCTTGGGCTCTTCTCTCCCAACGCACTTCAGGAG 788
QY 2502 CATCTGAGTCTTTTGTGGAAGGGATATGGACAGCAAGCATCCATGATTCATATCAT 2561
Db 789 CACATCGCTCTCGTGTCTTGGAGGGCGTGTGGACGACAAACATCCACGACTGCATTAC 848
QY 2562 GGTAAACATCTGGCCTATAATAGGTGAGGATACCATACCATACCAATCAACATACAAG 2621
Db 849 GCGAAGGTATGGCCAGTCTATGGGCGCTGGGTATCACNNACATCCACATACGACTTTACGC 908
QY 2622 CATACATATGGTCATTTATACCATATGATGAGTGGATGCTTTGGCTCTCT 2671
Db 909 CACAACATATGGGCACTACACCGTGTGGATGGAGTGTGATGTTGGTACGCT 958

RESULT 7

US-09-313-294A-4514
; Sequence 4514, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4514
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348549H1

US-09-313-294A-4514

Query Match 4.0%; Score 118.4; DB 3; Length 300;
Best Local Similarity 70.5%; Pred. No. 1.7e-20;
Matches 196; Conservative 0; Mismatches 76; Indels 2; Gaps 2;
QY 2408 GTTTTCAGGCTCGCATTCATTCGCTGGACGGGATCTTACGGCTATACCGCACGTGAT 2467
Db 10 GTTTGTGGACTCGCGTTTTTACCACCTGGATGGTATTTCTGCAAGCGATACCGCATGTCT 69
QY 2468 AGCGGTGTTTATAGTGGCGATTCATCTCATACACATCTGAGTCTTTTGTGGAAGG 2527
Db 70 TCGGCTCTTCTCTCCCAACGCACTTCAGGAGGACATTCGCTCTCGTGTCTTGGAGGG 129
QY 2528 GATATGGACAGCAAGCATCCATGATTCATATGATGATAATATGCGCTCTATATGGGTGC 2587
Db 130 CGTGTGGACGACAAACATCCACGCTGATTCAGGCAAGGTATGGCCAGTCTATGGCGCG 189
QY 2588 AGGATACCATACCATACCATACCAATACCAAGCATATGATGGTCATTTATACCATATG 2647
Db 190 TGGGTATCACACCATCCACATACGA-TTACCGCCCAACATATGGCCATACA-CGTCTG 247

QY 2648 GATGGACTGGATGTTTGGCTCTCT 2671
Db 248 GATGGACTGGATGTTTGGTACGCT 271

RESULT 8

US-09-313-294A-379
; Sequence 379, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 379
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 7005491111H1
; NAME/KEY: unsure
; LOCATION: 5
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-379

Query Match 3.1%; Score 90.8; DB 3; Length 269;
Best Local Similarity 65.0%; Pred. No. 2e-13;
Matches 134; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 2125 GAGCATGGTTGACCAAAATGTTACTCTACACTTGACCAATTCACACTGGTTCCTCTGTTTC 2184
Db 6 GAGCGGATGGGAACCGGTGTACTTTAATATCAGCGAAATGGGTTTTCTCGGTACCTT 65
QY 2185 CTCACATAGCTCTCTATCTCTTTAGTTAGTTATGTTATGTTTGGTTTCAAAAGAG 2244
Db 66 TGTATATAGCTATGATCTCATCTTTTGTGGAGTTTGGAAATTTACTGGATGCACAGAG 125
QY 2245 CTTCTATGACATTAATTTCTCTATAGCATCTCCATCTGCTACCATCATATGTATACAAAG 2304
Db 126 TTGCATGATTAAGCCACTATACAAACATCTGCTGACCCACCAATTTTACAAAG 185
QY 2305 CAAACACACTCTCTCCATTTCCCGG 2330
Db 186 GAGAACACCTTGCTCCGTTTGTGG 211

RESULT 9

US-09-443-041A-13
; Sequence 13, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 459
; TYPE: DNA

; ORGANISM: Glycine max
US-09-443-041A-13

Query Match 3.1%; Score 90; DB 3; Length 459;
Best Local Similarity 66.8%; Pred. No. 4.1e-13;
Matches 143; Conservative 0; Mismatches 70; Indels 1; Gaps 1;
QY 1524 GATTATAATGATCAGATCGTCAATGAGACCTCTTTTACACCGAATGGTTCTTGAGTCAC 1583
Db 100 GAATATTGAGGCTGTTCGGCGAAGACACGAGACTTGTACAACCGCATTCGTGTGGCGGC 159
QY 1584 CTTTTCGGGTGAATCTATGGGAACCTTTACACATTTCTCCAGACATGGCTCCGGAAC 1643
Db 160 CTATTGCGGCACTCTGTGTGGGCGCACTCCGCGCTTCTCCAGACGTGGTTCGCAAT 219
QY 1644 TACCTCGCGGAAACATACTCTACTTCTATCTCCGCTTCTCTGGTGTCTTACATCTAT 1703
Db 220 TACCTCGGCGGTCTCTCTACTCTCTCTCTGCGCTCTCTGCTGTGCTTCTACATTTAT 279
QY 1704 TA-CCTTAAACTCAACGTTTACGTCCCAAGGT 1736
Db 280 TATTGGGAAGCGCAAGTTTCATGTCCCAAGAT 313

RESULT 10

US-09-313-294A-7458
; Sequence 7458, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7458
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381763H1
US-09-313-294A-7458

Query Match 2.8%; Score 82.8; DB 3; Length 314;
Best Local Similarity 60.8%; Pred. No. 2.4e-11;
Matches 135; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 1520 GGCAGATTATAATGATCAGATCGTCAATGAGACCTCTTTTACACCGAATGGTTCTGAG 1579
Db 37 GCGGACTACCTTTGGCGGTTCTGTGGCGGAGACAGAGTGTACAAAGAGTTGTCTCAG 96
QY 1580 TCACCTTTTGGCGGTGAATCTATGGGAACCTTTTACACATTTCTCCAGACATGGCTCCG 1639
Db 97 CGCGTGGCGCAGCGACTGTGTGGCGGCTGCGCACCGGTGCTGATGATGCG 156
QY 1640 GAATACCTCGCGGAAACATCTACTTCTATCTCCGCTTCTCTGCTGTCTTACAT 1699
Db 157 CAACTCGCTCGCGGTACTCTCTCTATTTCTCTGCTGTCTCTGCTGTCTGCTCAT 216
QY 1700 CTATTACCTTAACTCAACGTTTACGTCCCAAGGTACTT 1741
Db 217 CTACTACTGGAAGCGCCACGCTCATATCCCAAGATGCCAT 258

RESULT 11

US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

	1736	473	1796	413	1856	353	1916	293	1976	233
Qy	TTACTCTTTTCAATTCGATGTCCTGTTCTTTTGAACCTTCTTTTGTGTGATTCCTTCGATT		GTATCGCCTGATAGATGCTTATPACGTTTAAACCTTTTCTTACTGTTACTTTTCAGTTC		TGTGCTCTACTCTCTCAATTTAAATAGTCTTTTAAAGTCTTAAATATTTTGGCTAAATCCACATT		TTTTAGTGGAACTCTCCATGAAATTTGAGCTGAAATATACCAATGAAATGAAATTTGTT		GGTCTTAGTTCATTTCTTGCTGGTTCTCTCTATTTTGTGGTT	
Db		TTTTTTTTTATTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT		ATTTTTTTTTTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT		TTTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT		TTTTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT		TTTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
Qy	414	1855	354	1915	294	1975	234			
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
Db										
Qy	1796	413	1856	353	1916	293	1976	233		
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
Db										
Qy	1796	413	1856	353	1916	293	1976	233		
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
Db										
Qy	1796	413	1856	353	1916	293	1976	233		
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Qy	1795	414	1855	354	1915	294	1975	234		
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Qy	1796	413	1856	353	1916	293	1976	233		
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
Db										
Qy	1796	413	1856	353	1916	293	1976	233		
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Qy	1795	414	1855	354	1915	294	1975	234		
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Qy	1796	413	1856	353	1916	293	1976	233		
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Qy	1795	414	1855	354	1915	294	1975	234		
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Qy	1796	413	1856	353	1916	293	1976	233		
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
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Qy	1796	413	1856	353	1916	293	1976	233		
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Qy	1795	414	1855	354	1915	294	1975	234		
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Qy	1796	413	1856	353	1916	293	1976	233		
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
Db										
Qy	1796	413	1856	353	1916	293	1976	233		
Db										
Qy	1795	414	1855	354	1915	294	1975	234		
Db										

NAME/Seq: unsure	2.1%;	Score 60.6;	DB 3;	Length 614;	
LOCATION: (1)..(614)	Best Local Similarity	50.2%;	Pred. No. 1.7e-05;		
OTHER INFORMATION: unsure at all n locations	Matches 150;	Conservative 0;	Mismatches 149;	Indels 0;	Gaps 0;
US-09-902-540-1318					
Qy	1736	TTACTTTTTTCAAAATTCGATGTTCTGTTTTTGAAACCTTCTCTTTTGTTGATTCCTTCGATT	1795		
Db	600	TTTTCTTTTTTTGATTTCTCTTTTTTTTGTTGTTCTTTCTTTTCTTCTCTCTCTGT	541		
Qy	1796	GTATCGCCTGATAGATTGGGTTATAGGTTAAACCTTTTTTTTCTTACTGTTACTTTTCAGTTC	1855		
Db	540	GTATTATTTTTTTTGTTGTTTTTTTT	481		
Qy	1856	TTGCTCTTCTACTCTCATTTTAAATAGTTTTTAAAGTTTAAATATTTTGGCTAAATCCACATT	1915		
Db	480	TTCTTTTTTTGTT	421		
Qy	1916	TTTTTAAGTTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTTGAAATTTGT	1975		
Db	420	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATGTTTTTTTGTGTTGTTTTTTT	361		
Qy	1976	GGTCTTAGTTCATTTCTTGCTGGTTCTTCTCTATTTTTTTGGTGTAGAAATCCATTCCT	2034		
Db	360	GTATTTTTTTTTTTATTTTTGTTTTTGTTTTTTTTTTTTTTTTTTTTTTTGCTTCTTTTTTTTTTCT	302		

Search completed: March 7, 2006, 13:20:15
Job time : 509 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:24:36 ; Search time 2072 Seconds
(without alignments)
11673.712 Million cell updates/sec

Title: US-10-736-318-22
Perfect score: 2925
Sequence: 1 gttgtgattattggtgc.....tcaaatggactaaatctg 2925

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2925	100.0	2925	3	US-09-775-879-22
2	2925	100.0	2925	7	US-10-736-318-22
3	924.4	31.6	1889	3	US-09-775-879-20
4	924.4	31.6	1889	7	US-10-736-318-20
5	461	15.8	1175	3	US-09-885-723-23
6	461	15.8	1175	9	US-10-862-907-23
7	347.2	11.9	846	3	US-09-938-842A-421
8	347.2	11.9	846	3	US-09-938-842A-421
9	203.4	7.0	1447	6	US-10-224-880C-27
10	200.8	6.9	1253	7	US-10-767-701-13122
11	189.4	6.5	833	6	US-10-259-194A-287
12	188	6.4	1135	6	US-10-259-194A-530
13	188	6.4	1210	6	US-10-224-880C-29
14	187	6.4	911	6	US-10-224-880C-23
15	184.4	6.3	828	6	US-10-259-194A-608
16	179.6	6.1	825	7	US-10-395-463-33
17	179.6	6.1	1318	6	US-10-224-880C-25
18	173.8	5.9	1070	6	US-10-224-880C-9
19	151.8	5.2	635	6	US-10-259-194A-422
20	142.4	4.9	699	7	US-10-425-114-24729
21	106	3.6	754	7	US-10-424-593-66086
22	104.6	3.6	285	3	US-09-294-093B-1568
23	93.4	3.2	404	7	US-10-425-114-5986

ALIGNMENTS

RESULT 1

US-09-775-879-22
; Sequence 22, Application US/09775879
; Patent No. US2002006822A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/09/775,879
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Genomic HDF7
US-09-775-879-22

Query Match	100.0%;	Score 2925;	DB 3;	Length 2925;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 2925;	Conservative	0;	Mismatches	0;	
		Indels	0;	Gaps	0;
QY	1	GTTTGGTATTATTGGATGCACAGAGCTTCATGACATTAGCCTCTCTATAAGTATCT	60		
DB	1	GTTTGGTATTATTGGATGCACAGAGCTTCATGACATTAGCCTCTCTATAAGTATCT	60		
QY	61	CCATGCCACCCATCATATCTPACAAACAGCAGAAATACACTCTCTCCATTGCCGGTAAAGTG	120		
DB	61	CCATGCCACCCATCATATCTPACAAACAGCAGAAATACACTCTCTCCATTGCCGGTAAAGTG	120		
QY	121	TTTTTCAGTTTGTCTTCTTTAGTTCCTTGTAAAAGATTGGTAGCATTTAGTTTCTTTACCAG	180		
DB	121	TTTTTCAGTTTGTCTTCTTTAGTTCCTTGTAAAAGATTGGTAGCATTTAGTTTCTTTACCAG	180		
QY	181	AAAAGACATTTGTTCAGCAGCTGCTGTACTCCAAATCACATTTTGCATTCCTTATCCATAA	240		
DB	181	AAAAGACATTTGTTCAGCAGCTGCTGTACTCCAAATCACATTTTGCATTCCTTATCCATAA	240		
QY	241	AGTAAACCAAGAGGCTAGAAATATATAAATGTGCAGCTGCATTACTTACATATGTCAGAG	300		
DB	241	AGTAAACCAAGAGGCTAGAAATATATAAATGTGCAGCTGCATTACTTACATATGTCAGAG	300		
QY	301	AGACTTCTGACTTAAACACAGAGTTTAGATCTTTGTGTGTTTCTCTTCTGCTCGGACTGATT	360		

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301 AGACTTCTGACTTAAACGAGTTTAGATCTTTGTGTTCTCTCTGGTCTCGGACTGTT 360
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361 GGAATGACGAGAGTTCTTTTATCTACTTCCCTGGAGTGTATCTTGGTTAATCCAAAGG 420
361 GGAATGACGAGAGTTCTTTTATCTACTTCCCTGGAGTGTATCTTGGTTAATCCAAAGG 420
|||||
421 TGTGACATCTAAATATTAATCTTGAACCTTCTTAAGTTTGTGTTTACAGGCTTGCATTCA 480
421 TGTGACATCTAAATATTAATCTTGAACCTTCTTAAGTTTGTGTTTACAGGCTTGCATTCA 480
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481 CCCAGTAGCGGATACTTAAAGCTGTACCGCATGTGATAGCGCTGTATAGTGCCTT 540
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DB 2521 TCGAAGGGATATGGACAGCAAGCATCCATGATTGTCATACATGGTAACATCTGGCCTATAA 2580
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DB 2821 TAATTTGATGCAAGTTTCAGACTTTTATTTGCTAAAAATCTCTGATGATTATTAACCTCA 2880
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DB 2881 ATTATATAATTCGTGATGAAGAGTTCAAATTTGGACTAAATCTG 2925

RESULT 2

US-10-736-318-22
; Sequence 22, Application US/10736318
; Publication No. US20040133948A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/10/736,318
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US/09/775,879
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Genomic HDF7
US-10-736-318-22

Query Match 100.0%; Score 2925; DB 7; Length 2925;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GTTTGGTATTATTGGATGCGACAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT 60
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DB 61 CCATGCCACCCATCATATCTACAACAGCAGAAATACACTCTCTCCATTTGGCGGTAAGTG 120
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DB 121 TTTTCAGTTGTTCTCTTTAGTTCTTTGTAAGATGTTAGTATTTAGTTCTTACCG 180
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DB 301 AGACTTCTGACTTAACACAGAGTTTATAGTCTTTTGTCTCTCTCTCTCTCTCTCTCTCTCT 360
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DB 421 TGTGACATCTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
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DB 481 CCCAGTAGACGGGATACCTTAAGGCTGTACCGCATGTAGCGCTGTGTATAGTGGCCAAAT 540
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DB 601 GACTGCATCTCATGGCAACATCTGGCCAGTAATGGGTGACAGGATACCATACGATACACAC 660
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US-09-775-879-20
; Sequence 20, Application US/09775879
; Patent No. US20020068822A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/09/775,879
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Genomic dwf7 (Arabidopsis)
US-09-775-879-20
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Query Match 31.6%; Score 924.4; DB 3; Length 1889;
Best Local Similarity 99.6%; Pred. No. 5.6e-204;
Matches 958; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Db 989 CCATGCCCAACCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCGGGAAGTG 1048
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Qy 181 AAAAGACTTTTGTGACAGCTGCTTGTACTCTCAAAATCACATTTTTCATTCATATAA 240
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QY 959 GC 960
Db 1888 GC 1889
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RESULT 4

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US-10-736-318-20
; Sequence 20, Application US/10736318
; Publication No. US20040133948A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/10/736,318
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US/09/775,879
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 20
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Genomic dwf7 (Arabidopsis)
US-10-736-318-20

Query Match 31.6%; Score 924.4; DB 7; Length 1889;
Best Local Similarity 99.6%; Pred. No. 5.6e-204;
Matches 958; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 1 GTTTCGTTATTTATTCGATGCACAGAGAGCTTCATGACATTTAAGCCCTCTCTATAAGTATCT 60
Db 929 GTTTCGTTATTTATTCGATGCACAGAGAGCTTCATGACATTTAAGCCCTCTCTATAAGTATCT 988
QY 61 CCATGCCACCCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCCGGTAAGTG 120
Db 989 CCATGCCACCCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCCGGTAAGTG 1048
QY 121 TTTTCAGTTTGTCTCTTTAGTTCTTTGTAAGAATTTGTTAGTATTTAGTTTCTTACCAG 180
Db 1049 TTTTCAGTTTGTCTCTTTAGTTCTTTGTAAGAATTTGTTAGTATTTAGTTTCTTACCAG 1108
QY 181 AAAAGACTTGTGACGAGCTGCTGTAATATATAAATGTGACGCTGATTTTGCATTCCTTATCAA 240
Db 1109 AAAAGACTTGTGACGAGCTGCTGTAATATATAAATGTGACGCTGATTTTGCATTCCTTATCAA 1168
QY 241 AGTAACCCAGAAAGGCTAGAAATATATAAATGTGACGCTGATTTTGCATTTACATATGTCAGAG 300
Db 1169 AGTAACCCAGAAAGGCTAGAAATATATAAATGTGACGCTGATTTTGCATTTACATATGTCAGAG 1228
QY 301 AGACTTCTGACTTAACAGAGTTAGATCTTTGTGTTTCTCTCTGCTCGGACTGATT 360
Db 1229 AGACTTCTGACTTAACAGAGTTAGATCTTTGTGTTTCTCTCTGCTCGGACTGATT 1288
QY 361 GGAATGACGAGAGTTCTTTATCTACTTCCCTGAGTGTATCTTGGTTAATCCAGGA 420
Db 1289 GGAATGACGAGAGTTCTTTATCTACTTCCCTGAGTGTATCTTGGTTAATCCAGGA 1348
QY 421 TGTGACATCTAAATATTAATCTGTAATCTCTTACGTTTGTGTTTACAGGCTTGCA - TTC 479
Db 1349 TGTGACATCT - AATATTAATCTGTAATCTCTTACGTTTGTGTTTACAGGCTTGCA 1407
QY 480 ACCAGTAGACGGGATACCTAAGGCTGTACCGCATGTGATGCGCTG - TTATAGTGCCAA 538
Db 1408 ACCAGTAGACGGGATACCTAAGGCTGTACCGCATGTGATGCGCTGTTTATAGTGCCAA 1467
QY 539 TTCATTTCAACTCATATAGTCTTTTGTCTTCTGTAAGCGGATATGGAAGCGGACATCC 598
Db 1468 TTCATTTCAACTCATATAGTCTTTTGTCTTCTGTAAGCGGATATGGAAGCGGACATCC 1527
QY 599 ATGACTGCATCCATGSCAACATCTGGCCAGTAAATGGTGCAGGATACCATACGATACACC 658
Db 1528 ATGACTGCATCCATGSCAACATCTGGCCAGTAAATGGTGCAGGATACCATACGATACACC 1587
QY 659 ACACGACATACAAAGCATACTATGCTCATTTATACCATATGGATGGATGTTTGGCT 718
Db 1588 ACACGACATACAAAGCATACTATGCTCATTTATACCATATGGATGGATGTTTGGCT 1647
QY 719 CTCCTAGGATCCTCTCTTAGAAGAGATGACAAACAGACAGCTTCAAGAAAGCAGAT 778
Db 1648 CTCCTAGGATCCTCTCTTAGAAGAGATGACAAACAGACAGCTTCAAGAAAGCAGAT 1707
QY 779 GAGAATGCCACTTGGGTTTTGTTCTTCTGTTTGTCTGTTGTTGTTTCAAGTT 838
Db 1708 GAGAATGCCACTTGGGTTTTGTTCTTCTGTTTGTCTGTTGTTGTTTCAAGTT 1767
QY 839 TCAGCCTTTCTGTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 898
Db 1768 TCAGCCTTTCTGTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1827
QY 899 ATTATATTGTTACAAACATTTGCTGCTAGTTTAAACATGTAATGTTTGTATGATCTTT 958
Db 1828 ATTATATTGTTACAAACATTTGCTGCTAGTTTAAACATGTAATGTTTGTATGATCTTT 1887
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QY 959 GC 960
Db 1888 GC 1889

RESULT 5
US-09-885-723-23
; Sequence 23, Application US/09885723
; Publication No. US20030150008A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS
; FILE REFERENCE: MTC6783.1
; CURRENT APPLICATION NUMBER: US/09/885,723
; CURRENT FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-885-723-23

Query Match 15.8%; Score 461; DB 3; Length 1175;
Best Local Similarity 97.6%; Pred. No. 2.3e-96;
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 462 TTTACAGGCGTTGCA-TTCACCCAGTAGCGGATACCTTAAGCTCTGTACCGCATGTGATA 520
Db 643 TTTGCGGGCGTTGCAATTTCAACCCAGTAGCGGATACCTTCAGGCTGTACCGCATGTGATA 702

QY 521 GCGCTG-TTATAGTGCCAAATTCATTTCAACAATCATATAGGCTTTTGTTCATGGAGCG 579
Db 703 GCGCTGTTTATAGTGCCAAATTCATTTCAACAATCATATAGGCTTTTGTTCATGGAGCG 762

QY 580 ATATGACGCGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 639
Db 763 ATATGGGCGGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 822

QY 640 GGATACCATACGATACACACACGACATCAAGCATTAATAGTCTATATACCATATGG 699
Db 823 GGATACCATACGATACACACACGACATCAAGCATTAATAGTCTATATACCATATGG 882

QY 700 ATGGATGTGATGTTGGCTCTCTTAGGGATCCCTCTTAGAGAGATCCCTCTTAGAGAGATGACACAAAGAC 759
Db 883 ATGGATGTGATGTTGGCTCTCTTAGGGATCCCTCTTAGAGAGATCCCTCTTAGAGAGATGACACAAAGAC 942

QY 760 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACATCTGGGTTTGTCTCTGTTTGTCTTGT 819
Db 943 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACATCTGGGTTTGTCTCTGTTTGTCTTGT 1002

QY 820 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTTCTCTTCTCTTCTCTTCTTCTTCTTCT 879
Db 1003 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTTCTCTTCTCTTCTCTTCTTCTTCTTCT 1062

QY 880 GTCTCTCAACCTTTCCAAATTAATGTTACAAACATTTGCTGTCTAGTTTAAACATG 939
Db 1063 GTCTCTCAACCTTTCCAAATTAATGTTACAAACATTTGCTGTCTAGTTTAAACATG 1122

QY 940 TAAATGTTTGATCATCTTTGC 960
Db 1123 TAAATGTTTGATCATCTTTCC 1143

RESULT 6
US-10-862-907-23
; Sequence 23, Application US/10862907
; Publication No. US20050086713A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS
; FILE REFERENCE: MTC6783.1
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; CURRENT APPLICATION NUMBER: US/10/862,907
; CURRENT FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: US/09/885,723
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-862-907-23

Query Match 15.8%; Score 461; DB 9; Length 1175;
Best Local Similarity 97.6%; Pred. No. 2.3e-96;
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 462 TTTACAGGCGTTGCA-TTCACCCAGTAGCGGATACCTTAAGCTGTGTACCGCATGTGATA 520
Db 643 TTTGCGGGCGTTGCAATTTCAACCCAGTAGCGGATACCTTCAGGCTGTGTACCGCATGTGATA 702

QY 521 GCGCTG-TTATAGTGCCAAATTCATTTCAACAATCATATAGGCTTTTGTTCATGGAGCG 579
Db 703 GCGCTGTTTATAGTGCCAAATTCATTTCAACAATCATATAGGCTTTTGTTCATGGAGCG 762

QY 580 ATATGACGCGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 639
Db 763 ATATGGGCGGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 822

QY 640 GGATACCATACGATACACACACGACATCAAGCATTAATAGTCTATATACCATATGG 699
Db 823 GGATACCATACGATACACACACGACATCAAGCATTAATAGTCTATATACCATATGG 882

QY 700 ATGGATGTGATGTTGGCTCTCTTAGGGATCCCTCTTAGAGAGATCCCTCTTAGAGAGATGACACAAAGAC 759
Db 883 ATGGATGTGATGTTGGCTCTCTTAGGGATCCCTCTTAGAGAGATCCCTCTTAGAGAGATGACACAAAGAC 942

QY 760 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACATCTGGGTTTGTCTCTGTTTGTCTTGT 819
Db 943 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACATCTGGGTTTGTCTCTGTTTGTCTTGT 1002

QY 820 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTTCTCTTCTCTTCTCTTCTTCTTCTTCT 879
Db 1003 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTTCTCTTCTCTTCTCTTCTTCTTCTTCT 1062

QY 880 GTCTCTCAACCTTTCCAAATTAATGTTACAAACATTTGCTGTCTAGTTTAAACATG 939
Db 1063 GTCTCTCAACCTTTCCAAATTAATGTTACAAACATTTGCTGTCTAGTTTAAACATG 1122

QY 940 TAAATGTTTGATCATCTTTGC 960
Db 1123 TAAATGTTTGATCATCTTTCC 1143

RESULT 7
US-09-938-842A-421
; Sequence 421, Application US/09938842A
; Patent No. US20030160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
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; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 421
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-421

Query Match      11.9%; Score 347.2; DB 3; Length 846;
Best Local Similarity 72.4%; Pred. No. 5.7e-70;
Matches 508; Conservative 0; Mismatches 108; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATATAGTGGCAATGAAGCTAT 2081
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 AGATGCAATTCCTACAAATAAAGGCTATGCGTTTGCAAATGTTTGTGGCAATGAAGCTAT 284

QY 2082 GCCTTGGTACACTCTCTTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 GCATGGTACACTCTCTTCCAACTGCTCCGAGAGTATGATGAACGTGGTTGGACCAA 344

QY 2142 ATGTTACTCTACACTTGACCAATTTCAACTGGTTCTCTCTCTCTACATAGCTCTCTA 2201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 ATGTTTGTCTAGCATAGGCGAATTCGGCTGGATTCGTATTTTGTACATGCCATCTA 404

QY 2202 TCTTGTTTTAGTGGTTTATGATTTATTTGGGTTTCAAAAGCTTCATGACATTAAT 2261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TCTTGTTTTGTGAGTTTGGTATTTATTTGGATGACAGAGCTTCATGACATTAAGCC 464

QY 2262 TCTCTAAGCATCTCCATGCTACCCATCATATGTACAAAGCAAGCAAAACACACTCTCTCC 2321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 TCTCTAAGTATCTCCATGCGCCACCCTCATATCTACAAAGCAAGCAATACACTCTCTCC 524

QY 2322 ATTTGCCGATATGTCAAAGCTATATGTTCTCAATCTAAATTCAAAGCTTGTATCAATGG 2381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 ATTTGCC----- 531

QY 2382 TGACTTCTTTACTTGATGTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGGG 2441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 -----GGGCTTGCATTTTCAACCAGTAGACGGG 558

QY 2442 ATACTTCAGGCTATACCGCACTGATAGCGCTGTTTATAGTCGCGATTCATCTCATACA 2501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 559 ATACTTCAGGCTGATCCGATGATAGCGCTGTTTATAGTCCCAATTCATTTCAACT 618

QY 2502 CATCTGAGTCTTTTGTGTTGGAAGGATATGACAGCAAGCATCCATGATTCATACAT 2561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 CATATAGTCTTTTGTTCATGAGCGATATGACGCGCAACATCCATGACTGCATCCAT 678

QY 2562 GGTAAACATCTGGCCTATTAATGGTGCAGGATACCATACATACACCATACAACATACAAG 2621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 GGCACACATCTGGCCAGTAAATGGGTGCAGGATACCATACATACACCATACAACATACAAG 738

QY 2622 CATAACTATGTCATTAACCATATGATGGATGGATGTTGGCTCTCTTATGGTCTCT 2681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 CATAACTATGTCATTAACCATATGATGGATGGATGTTGGCTCTCTTATGGGATCCT 798

QY 2682 TTAGCAGAAAAGACAGTTTCAAGGAGAAAGAAAGTGAGAA 2723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 CTCTTAGAAGATGACAAACAGACAGCTTCAAGAAAGCA 840

RESULT 8
US-09-938-842A-421
; Sequence 421, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
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; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 421
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-421

Query Match      11.9%; Score 347.2; DB 3; Length 846;
Best Local Similarity 72.4%; Pred. No. 5.7e-70;
Matches 508; Conservative 0; Mismatches 108; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCCTACGAGAAAGGCAATGCTTTTGCAAATATATAGTGGCAATGAAGCTAT 2081
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 AGATGCAATTCCTACAAATAAAGGCTATGCGTTTGCAAATGTTTGTGGCAATGAAGCTAT 284

QY 2082 GCCTTGGTACACTCTCTTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 GCCATGGTACACTCTCTTCCAACTGCTCCGAGAGTATGATGAACGTGGTTGGACCAA 344

QY 2142 ATGTTACTCTACACTTGACCAATTTCAACTGGTTCTCTCTCTCTACATAGCTCTCTA 2201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 ATGTTTGTCTAGCATAGGCGAATTCGGCTGGATTCGTATTTTGTACATGCCATCTA 404

QY 2202 TCTTGTTTTAGTGGTTTATGATTTATTTGGGTTTCAAAAGCTTCATGACATTAAT 2261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TCTTGTTTTGTGAGTTTGGTATTTATTTGGATGACAGAGCTTCATGACATTAAGCC 464

QY 2262 TCTCTAAGCATCTCCATGCTACCCATCATATGTACAAAGCAAGCAAAACACACTCTCTCC 2321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 TCTCTAAGTATCTCCATGCGCCACCCTCATATCTACAAAGCAAGCAATACACTCTCTCC 524

QY 2322 ATTTGCCGATATGTCAAAGCTATATGTTCTCAATCTAAATTCAAAGCTTGTATCAATGG 2381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 ATTTGCC----- 531

QY 2382 TGACTTCTTTACTTGATGTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGGG 2441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 -----GGGCTTGCATTTTCAACCAGTAGACGGG 558

QY 2442 ATACTTCAGGCTATACCGCACTGATAGCGCTGTTTATAGTCGCGATTCATCTCATACA 2501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 559 ATACTTCAGGCTGATCCGATGATAGCGCTGTTTATAGTCCCAATTCATTTCAACT 618

QY 2502 CATCTGAGTCTTTTGTGTTGGAAGGATATGACAGCAAGCATCCATGATTCATACAT 2561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 CATATAGTCTTTTGTTCATGAGCGATATGACGCGCAACATCCATGACTGCATCCAT 678

QY 2562 GGTAAACATCTGGCCTATTAATGGTGCAGGATACCATACATACACCATACAACATACAAG 2621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 GGCACACATCTGGCCAGTAAATGGGTGCAGGATACCATACATACACCATACAACATACAAG 738

QY 2622 CATAACTATGTCATTAACCATATGATGGATGGATGTTGGCTCTCTTATGGTCTCT 2681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 CATAACTATGTCATTAACCATATGATGGATGGATGTTGGCTCTCTTATGGGATCCT 798

QY 2682 TTAGCAGAAAAGACAGTTTCAAGGAGAAAGAAAGTGAGAA 2723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 CTCTTAGAAGATGACAAACAGACAGCTTCAAGAAAGCA 840

RESULT 9
US-10-224-880C-27
; Sequence 27, Application US/10224880C
; Publication No. US20030229914A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
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Qy	2683	TAG 2685	
Db	811	AAG 813	
RESULT 12			
US-10-259-194A-530			
; Sequence 530, Application US/10259194A			
; Publication No. US20040010815A1			
; GENERAL INFORMATION:			
; APPLICANT: Lange, Markus B.			
; APPLICANT: Ghassemlan, Majid			
; APPLICANT: Briggs, Steven P.			
; APPLICANT: Cooper, Bret			
; APPLICANT: Glazebrook, Jane			
; APPLICANT: Goff, Stephen A.			
; APPLICANT: Katagiri, Rumiaki			
; APPLICANT: Kreps, Joel			
; APPLICANT: Moughamer, Todd			
; APPLICANT: Provart, Nicholas			
; APPLICANT: Ricke, Darrell			
; APPLICANT: Zhu, Tong			
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES			
; FILE REFERENCE: 70029-NP			
; CURRENT APPLICATION NUMBER: US/10/259,194A			
; CURRENT FILING DATE: 2003-01-07			
; PRIOR APPLICATION NUMBER: US 60/325,277			
; PRIOR FILING DATE: 2001-09-26			
; PRIOR APPLICATION NUMBER: US 60/370,743			
; PRIOR FILING DATE: 2002-04-04			
; PRIOR APPLICATION NUMBER: US 60/370,620			
; PRIOR FILING DATE: 2002-04-04			
; NUMBER OF SEQ ID NOS: 662			
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta			
; SEQ ID NO 530			
; LENGTH: 1135			
; TYPE: DNA			
; ORGANISM: Triticum aestivum			
US-10-259-194A-530			
Query Match 6.4%; Score 188; DB 6; Length 1135;			
Best Local Similarity 59.8%; Pred. No. 6.8e-33;			
Matches 389; Conservative 0; Mismatches 17; Indels 86; Gaps 1;			
Qy	2022	AGATCCATCTCTACGAGAAAGCAATGCTTTTGCAAATATACGTGCAATGAGGCTAT	2081
Db	220	AGATGTCGTCCCTACAGTGAAGCTATGAAGAGCAAAATAATTGTTGCATCAAGGCTAT	279
Qy	2082	GCCTTGGTACACTCTCTCTCCAGCTGCTCTGAGTATATGATCAGCATGCTTGGACCA	2141
Db	280	GCCTTTCTACTGTGCTCTTCCTCGTATCTGAGCACAATGATGAGAGTGGATGACACG	339
Qy	2142	ATGTTACTCTACACTTGACCAATTCACCTGGTTCTCTGTTTCTCTACATAGCTCTCTA	2201
Db	340	GTGTTTCTTTTCATATCAGCGAAGTTGGTTGGCCCTATGTATGATATCTATGTGCTCTATA	399
Qy	2202	TCTTGTGTTTGTAGTTGAGTTTATGATTTTATTTGGGTTTCAGAAAGCTTCATGACATTAAT	2261
Db	400	TCTCATCTTTGTGGAGTTCCGGAATTTACTGGATGCAAGAGTTGTCATGACATAAAGCC	459
Qy	2262	TCCTATAAGCATCTCCATGCTACCCATCATATGTATGTAACAACAGCAAAACACACTCTCTCC	2321
Db	460	ACTATACAGACCTTACATGCAACCCACCAATTTACACAGAGNATACCTTATCACC	519
Qy	2322	ATTTCGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTTGTATCAATGG	2381
Db	520	ATTTG-----	524
Qy	2382	TGACTTCTTTACTTGATGTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGGG	2441
Db	525	-----CTGGACTAGCAATTCCTATCCATTCATTCGAGCGG	553

QY 2442 ATACTTCAGGCTATACCGCAGGTGATAGCGCTGTTTATAGTCGCGATTTCATCTCATPAACA 2501
|||||
Db 554 ATACTCGAAGCCATATCGCAGGTGATGCTCTGTTCCCTTCCCGATGCACTTCAGGACG 613
|||||
QY 2502 CATCTGAGTCTTTTGTGGAAGGGATATGGACAGCAAGCATCCATGATTGCATACAT 2561
|||||
Db 614 CACATTGCTCTCTATTATAGAGCGGTGTGGACGGCAACATCCACGACTGCATCCAC 673
|||||
QY 2562 GGTAAACATCTGGCCTATATAGGTGAGGATACCATATACATACACCATCAACATACAAG 2621
|||||
Db 674 GGCAGATCTGGCCGGTGTATGGCGCGGTACACACCATCCACACGACGATACCGG 733
|||||
QY 2622 CATAACTATGTCATTATACCATATGATGGAGCTGGATGTTGGCTCTCT 2671
|||||
Db 734 CACAACATATGGCCACTACACCGTGTGGATGGACTGGCTGTTTGGCACCCCT 783
|||||

RESULT 13

US-10-224-880C-29
; Sequence 29, Application US/10224880C
; Publication No. US20030229914A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Emil M.
; APPLICANT: Rafaleki, J. Antoni
; APPLICANT: Shen, Jennie B.
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE: BB1282 US DIV
; CURRENT APPLICATION NUMBER: US/10/224,880C
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1130)
; OTHER INFORMATION: n = A, C, G, or T
US-10-224-880C-29

Query Match 6.4%; Score 188; DB 6; Length 1210;
Best Local Similarity 59.8%; Pred. No. 7e-33;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCTTACGAGAAAGCAATGCTTTTGCAAAATATAGTGGCAATGAAGGCTAT 2081
|||||
Db 188 AGATGCTGTCCTTACAGTAGAGCTATGAAGAGCAAAATATGTTGCATCAAGGCTAT 247
|||||
QY 2082 GCCTGGTACACTCTTCTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
|||||
Db 248 GCCTTTCTACTGTGCTCTCCGTCGCTATCTGAGCACATGATTGAGAGTGGATGGACAG 307
|||||
QY 2142 ATGTTACTTACACTTGACCAATTTCAACTGGTTCCTCTGTTCTCTACATAGCTCTCTA 2201
|||||
Db 308 GTGTTTCTTTTCATATCAGCGAAGTTGGTTGGCCTATGTATCATATATCTATGTCTCTATA 367
|||||
QY 2202 TCTGTGTTTATGTTGAGTTATGATTTATGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
|||||
Db 368 TCTCATCTTTGTGGAGTTTCGGAATTTATCTGGATGCAAGAGTTGCTGATGACATAAGCC 427
|||||
QY 2262 TCTCTATAAGCACTCTCCATGCTACCCATCATATGTACAACAGCAAAACACATCTCTCC 2321
|||||
Db 428 ACTATACAAGCACTCATACGCAACCCACCATTTTACAAAGGAGAATACCCCTATCACC 487
|||||
QY 2322 ATTTGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381
|||||
Db 488 ATTTG----- 492
QY 2382 TGACTCTTTTACTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCAATTCATCCGCTGGACGGG 2441
|||||

Db 493 -----CTGAGCTAGCATTTCCATCCATTGGACGGG 521
|||||
QY 2442 ATACTTCAGGCTATACCGCAGGTGATAGCGCTGTTTATAGTCGCGATTTCATCTCATPAACA 2501
|||||
Db 522 ATACTGCAAGCCATATCGCAGGTGATGCTCTGTTCCCTTCCCGATGCACTTCAGGACG 581
|||||
QY 2502 CATCTGAGTCTTTTGTGGAAGGGATATGGACAGCAAGCATCCATGATTGCATACAT 2561
|||||
Db 582 CACATTGCTCTCTATTATAGAGCGGTGTGGACGGCAACATCCACGACTGCATCCAC 641
|||||
QY 2562 GGTAAACATCTGGCCTATATAGGTGAGGATACCATATACATACACCATCAACATACAAG 2621
|||||
Db 642 GGCAGATCTGGCCGGTGTATGGCGCGGTACACACCATCCACACGACGATACCGG 701
|||||
QY 2622 CATAACTATGTCATTATACCATATGATGGAGCTGGATGTTGGCTCTCT 2671
|||||
Db 702 CACAACATATGGCCACTACACCGTGTGGATGGACTGGCTGTTTGGCACCCCT 751
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RESULT 14

US-10-224-880C-23
; Sequence 23, Application US/10224880C
; Publication No. US20030229914A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Emil M.
; APPLICANT: Rafaleki, J. Antoni
; APPLICANT: Shen, Jennie B.
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE: BB1282 US DIV
; CURRENT APPLICATION NUMBER: US/10/224,880C
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Zea mays
US-10-224-880C-23

Query Match 6.4%; Score 187; DB 6; Length 911;
Best Local Similarity 59.8%; Pred. No. 1e-32;
Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

QY 2023 GAATCCATTCTTACGAGAAAGCAATGCTTTTGCAAAATATAGTGGCAATGAAGGCTATG 2082
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Db 74 GATGCCATCCCCACAAATGAAGCTATGAAGAGCAAAATAGCTGTAGCATCCAAGGCTATG 133
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QY 2083 CTTTGGTACACTCTTCTTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2142
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Db 134 CTTTCTTTTACTGTGCTCTTCCAACTTTATCTGAGTATATGATCGAGAGTGGATGGACCCCG 193
|||||
QY 2143 TGTACTCTTACACTTGACCAATTTCAACTGGTTCCTCTGTTCTCTTACATAGCTCTCTAT 2202
|||||
Db 194 TGTACTTTTAAATATCAGCGAAATGGTTCCTGTCATACCTTGTATATGCTATGAT 253
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QY 2203 CTTGTTTATGTTAGTTTATGATTTATGGGTTTCAAAAGAGCTTCATGACATTAAT 2262
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Db 254 CTCATTTTGTGGAGTTTGGAAATTTACTGGATGCAAGAGAGTTGTCATGACATAAGCCA 313
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QY 2263 CTCATATAGCATCTCCATGCTACCCATCATATGTACACAGCAAAACACATCTCTCCA 2322
|||||
Db 314 CTATACAACATCTGCTGCGACCCCAACCATATTTTACAACAGGAGAACACCTTGTCTCCG 373
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QY 2323 TTTGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGGT 2382
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Db 374 TTTC----- 378
QY 2383 GACTCTTTTACTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCAATTCATCCGCTGGACGGGA 2442
|||||

Db 379 -----TGGACTCGGTTTCCACCCACTGGATGTA 407
QY 2443 TACTTCAGGCTATACCGCAGTGATAGCGCTGTTTATAGTGCAGATTCAATCTCATAAACAC 2502
Db 408 TTCTGCAAGGATACCGCATGCTTGGCTCTTCTCTCCCAACGCACTTCAGGACGC 467
QY 2503 ATCTGAGTCTTTTGGTGGTGGGATATGGACAGCAAGCATCCATGANTGGATACATG 2562
Db 468 ACATCGCTCTCGTGTCTTGGAGGGGCTGTGGACGACAAACATCCACGACTGCATTCAAG 527
QY 2563 GTAACATCTGGCTATAATGGGTGCAGGATACCATACCATACCATACATACATACATCAAGC 2622
Db 528 GCAAGGTATGGCCAGTCATGGGGGCTGGGTATCACACCATCCACCATACGACTTACCGCC 587
QY 2623 ATAACTATGGTCAATTATACCATATGATGGAGCTGGATGTTTGGCTCTCT 2671
Db 588 ACRACATATGCCACTACACCGTCTGGATGGACTGGATGTTTGGTACGCT 636

RESULT 15

US-10-259-194A-608
; Sequence 608, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Chasseman, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 608
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Zea mays
US-10-259-194A-608

Query Match 6.3%; Score 184.4; DB 6; Length 828;
Best Local Similarity 59.0%; Pred. No. 4e-32;
Matches 392; Conservative 0; Mismatches 186; Indels 86; Gaps 1;
QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGGCAATATAGTGGCAATGAAGCTAT 2081
Db 234 AGATGCCATCCCCACAAATGAAGCTATGAAGCAAAATAGTTGTAGCATCGAAGGCTAT 293
QY 2082 GCCTGTGACACTCTTCTTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141
Db 294 GCCTTTTACTGGGCTCTTCCAACTTTATCTGATATATGATGAGCGGATGGACTCG 353
QY 2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTTCTCTCTCTCTACATAGCTCTCTA 2201
Db 354 GAGCTACTTCGATATCAGCGAAATTCGTTTCTATGTACCTCTGTTATATGGCTATGA 413
QY 2202 TCTTGTTTTGTAGTTAGTTATGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
Db 414 TCTCATCTTTGTGGAGTTTGGAAATTTACTGGATGCAAGAGAGTTGTCATGACATAAAACC 473

QY 2262 TCTCTATAAGCATCTCCATGCTACCATCATATGTACAAAGCAAAACACACTCTCTCTCC 2321
Db 474 ATTATACAATATCTGCATGCAACCCACCATATTTTACACAAAGGAGATACCTTGTCTCC 533
QY 2322 ATTTGCCGATATGTCMAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTTGTATCAATGG 2381
Db 534 ATTTG----- 538
QY 2382 TGACTTCTTTTACTTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCATTTCCATCCGCTGGACGGG 2441
Db 539 -----CTGGACTTTGCATTTTCATTCACCTGGATGGT 567
QY 2442 ATACTTCAGGCTATACCGCACTGATAGCGCTGTTTATAGTGCAGATTCAATCTCATAAACA 2501
Db 568 GTTCTGCAAGCAATACCAACATGTTTCGGGCTCTTCTCTTTTCCAAAGCACTTCAGGACA 627
QY 2502 CATCTGAGTCTTTTGGTGGAGGGATATGGACAGCAAGCATCCATGATGTCATACAT 2561
Db 628 CATATTGCACTCTTGTTCCTAGAGGCTGTGTGGACAAACATCCACGACTGCATTCAT 687
QY 2562 GGTAAACATCTGGCCTATATATGGTGCAGGATACCATACCATACCATACCAACATCAAG 2621
Db 688 GGCAAGATATGGCCAGTCAATGGTGTCTGGATATCACCATTCACCATACGATACCCGC 747
QY 2622 CATAACTATGGTCAATTATACCATATGATGGAGTGGACTGGATGTTTGGCTCTCTTATGGTTCCT 2681
Db 748 CACAACTATGGCCACTACACCATCTGGATGGACTGGATGTTTGGTACGCTCAATGAGCCA 807
QY 2682 TTAG 2685
Db 808 GAAG 811

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Job time : 2080 secs

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:28:50 ; Search time 809 Seconds
(without alignments)
7927.094 Million cell updates/sec

Title: US-10-736-318-22
Perfect score: 2925
Sequence: 1 gtttggtatttggatgc.....tcaaatggactaaatctg 2925

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues
Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.2	1.9	3641	12	US-11-102-026A-181
2	53.8	1.8	305312	8	US-10-995-561-13236
3	52.8	1.8	8537	8	US-10-240-708-42
4	52	1.8	5562	8	US-10-240-708-63
5	51.6	1.8	6326	8	US-10-240-708-57
6	51.6	1.8	8607	8	US-10-240-708-72
7	51	1.7	828	6	US-09-925-065A-768903
8	50.8	1.7	664	6	US-09-925-065A-402424
9	50.8	1.7	664	6	US-09-925-065A-402425
10	50.2	1.7	5360	8	US-10-240-708-66
11	49.8	1.7	613	6	US-09-925-065A-834303
12	49.4	1.7	613	6	US-09-925-065A-834302
13	49.4	1.7	2409	8	US-10-821-234-2
14	49.4	1.7	5152	8	US-10-240-708-47
15	49.4	1.7	10166	12	US-11-147-606-3
16	49	1.7	560	6	US-09-925-065A-195994
17	49	1.7	560	6	US-09-925-065A-195995
18	49	1.7	6040	8	US-10-240-708-70
19	49	1.7	6801	8	US-10-240-708-62
20	48.8	1.7	524	6	US-09-925-065A-389544

21	48.8	1.7	562	6	US-09-925-065A-337713	Sequence 337713,
22	48.8	1.7	624	6	US-09-925-065A-749620	Sequence 749620,
23	48.8	1.7	624	6	US-09-925-065A-822274	Sequence 822274,
24	48.6	1.7	6317	8	US-10-240-708-12	Sequence 12, Appl
25	48.4	1.7	5455	8	US-10-240-708-34	Sequence 34, Appl
26	48	1.6	377	6	US-09-925-065A-599143	Sequence 599143,
27	47.8	1.6	8961	8	US-10-240-708-80	Sequence 80, Appl
28	47.6	1.6	4330	12	US-11-091-883-182	Sequence 182, Appl
29	47.4	1.6	6070	8	US-10-240-708-10	Sequence 10, Appl
30	47.2	1.6	1837	8	US-10-947-249-133	Sequence 133, Appl
31	47.2	1.6	1837	12	US-11-000-688-278	Sequence 278, Appl
32	47.2	1.6	5455	8	US-10-240-708-33	Sequence 33, Appl
33	47	1.6	1237	6	US-09-925-065A-714408	Sequence 714408,
34	47	1.6	1237	6	US-09-925-065A-714409	Sequence 714409,
35	47	1.6	1237	6	US-09-925-065A-714410	Sequence 714410,
36	47	1.6	1237	6	US-09-925-065A-714411	Sequence 714411,
37	47	1.6	8467	12	US-11-011-332A-96	Sequence 96, Appl
38	46.8	1.6	610	6	US-09-925-065A-939011	Sequence 939011,
39	46.8	1.6	8961	8	US-10-240-708-79	Sequence 79, Appl
40	46.8	1.6	10467	8	US-10-240-708-2	Sequence 2, Appl
41	46.8	1.6	19513	8	US-10-240-708-40	Sequence 40, Appl
42	46.6	1.6	591	6	US-09-925-065A-162822	Sequence 162822,
43	46.6	1.6	8607	8	US-10-240-708-71	Sequence 71, Appl
44	46.4	1.6	445	6	US-09-925-065A-808614	Sequence 808614,
45	46.4	1.6	8537	8	US-10-240-708-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-11-102-026A-181
; Sequence 181, Application US/11102026A
; Publication No. US20060021087A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Baum, James A
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Kovalic, David K
; APPLICANT: LaRosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Muniyika, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in P
; FILE REFERENCE: 38-21(53596)
; CURRENT APPLICATION NUMBER: US/11/102,026A
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60560842
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60565632
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60579062
; PRIOR FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60603421
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: 60617261
; PRIOR FILING DATE: 2004-10-11
; PRIOR APPLICATION NUMBER: 60669241
; PRIOR FILING DATE: 2005-04-07
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 181
; LENGTH: 3641
; TYPE: DNA
; ORGANISM: Lygus hesperus
US-11-102-026A-181

Query Match 1.9%; Score 54.2; DB 12; Length 3641;
Best Local Similarity 50.6%; Pred. No. 0.81;
Matches 131; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 1727 CCCCAAGGTACTTTTTCATTCGATGTCCTTTTGAACCTTTCTTTTGTGATT 1786

QY 1927 ATCTTCATGAATTTGAGCTCAAAATATACCATGAA-ATTGAAATTTGGTCTTAGT 1985
|||
Db 7110 ATATATTTTGTATAGTTGCTTTTGTGGAAGAAATAAAGAGGTTTATAGTAGTTG 7169
|||
QY 1986 TCTATTCTTGTGTTGTTCTTCTATATTTTGTGGTTAGAAATCCATT 2031
|||
Db 7170 TTTGTTTGTATTAGTTGTTTGTATAGAAAGTTTATTAGAAATAGTT 7215
|||

RESULT 7
US-09-925-065A-768903
; Sequence 768903, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 768903
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-768903

Query Match 1.7%; Score 51; DB 6; Length 628;
Best Local Similarity 51.7%; Pred. No. 2;
Matches 140; Conservative 1; Mismatches 126; Indels 4; Gaps 1;
QY 1654 GAAACATACCTCTACTCTCGGCTTCTCTGGTCTCTACATCTATTACCTTAAAC 1713
|||
Db 353 GTAATGATCAATTTTCAAGTCTGACTTTATGTAATCAATGCTCTATTAATTTAT 412
|||
QY 1714 TCAAGTTTACGTCCTCAAGGTTACTTTTTTCAATTTGAGTTCTGTTTGAACCTT 1773
|||
Db 413 TTTTAGTTAGTCTGGCTAAAAGTTTCTATTGTTTATCTTTGCTTCATTGA----TA 468
|||
QY 1774 TCTTTTGTGATTCCTTCGATTTGATCGCTGATAGATGTTGTTATACGTTAACCTTTT 1833
|||
Db 469 TTTTGTATGTTTCTTCTTGTGTTTCAATTTTCTGCTGCTGATCTTTATTTGT 528
|||
QY 1834 TCTTACTGTACTTTTCAGTCTGTCTCTACTCTCTCAATTAATTTAGTTTAAAGTTTA 1893
|||
Db 529 TTTCTTCTACTAATTTTGGTTAGTTGTTGTTGTTTCTGTTTCTTAATTTCTTAATGATC 588
|||
QY 1894 ATATTTTGGCTAATCCACATTTTAAAGTT 1924
|||
Db 589 ATAAAGTTGTTCAATGAAAGTTTCTTACTT 619
|||

RESULT 8
US-09-925-065A-402424/c
; Sequence 402424, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 402424
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-402424

Query Match 1.7%; Score 50.8; DB 6; Length 664;
Best Local Similarity 48.0%; Pred. No. 2.2; Mismatches 153; Indels 0; Gaps 0;
Matches 142; Conservative 1;
QY 1736 TTACTTTTTTCAATTTGATGTTCTGTTTGAACCTTTCTTTTGTGATTCCTTCGATT 1795
|||
Db 462 TGACTTTTTCAAAAACCAATTTTGTGTTGATCTTTTGTATTTTCTTTTAAAT 403
|||
QY 1796 GTATCGCCTGATAGATTTGTTATAGTTAACTTTTCTTACTGTTACTTTCAGTTT 1855
|||
Db 402 TCAATTTTCAATTTTCTGTCGACCTTTATTTTTTCTTACTAAATTTTGGGT 343
|||
QY 1856 TTGCTCTTCTACTCTCAATTTAATTTTAAAGTTTAAATTTTGGCTAATCCACAT 1915
|||
Db 342 TCTTTGCTCTTGCATTTCTAGTTCTTTAAGATGATCATTTAGATTTTATTTAAAT 283
|||
QY 1916 TTTTAAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTTGAT 1975
|||
Db 282 TTTTCTCTTTTGTGATGAGACATTTATAGCTATAAATTTCCCTCTCTAGTTCTGCTTTG 223
|||
QY 1976 GGTCTTAGTTCTATTCTTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2031
|||
Db 222 TGTATCTCAAGGTTTAAATACGTCATGTTTCCATTTATCATTTGTTTCAAGAAAT 167
|||

RESULT 9
US-09-925-065A-402425/c
; Sequence 402425, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 402425
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-402425

Query Match 1.7%; Score 50.8; DB 6; Length 664;
Best Local Similarity 48.0%; Pred. No. 2.2;
Matches 142; Conservative 1; Mismatches 153; Indels 0; Gaps 0;

QY 1736 TTACTTTTTCATTCGATGTCGTTTGAACCTTCTTTTGTGATCTCTTCGATT 1795
DB 462 TGACITTTCAAAACCAATTTTGTGTCGTTGATCTTTGTATTTTCTTTAAAT 403

QY 1796 GTATCGCTCATAGTGTGTATAGCTTAAACCTTTTCTTACTTGTACTTCAGTTC 1855
DB 402 TCAATTTATTTCTGTCGACCTTTATTTTCTTCTACTAATTTGGGT 343

QY 1856 TTGCTCTTCTACTCTCATTTAATAGTTTAAAGTTTAAATTTTGGCTAATCCACATT 1915
DB 342 TCGTTTGCCTTCGCAATTTCTAGTCTTTAAGATGCAATCATTTGTTTATTTAAAT 283

QY 1916 TTTTAAAGTTGAATCTCCATGAATTTGAGCTCAAAATATACATGAATGCAATTTGT 1975
DB 282 TTTTCTCTTTTGTATGATGACATTTATAGCTATAAATTTCCCTCTTAGTCTGCTTTG 223

QY 1976 GGTCTTCTAGTCTATTTCTGTTGTTTCTTCTATTTTGTGTTAGATCCATT 2031
DB 222 TGTATCTCAAGTTTATATAGCTCATGTTTCCATATCATTTGTTCAAGAAAT 167

RESULT 10
US-10-240-708-66
; Sequence 66, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-240-708-66

Query Match 1.7%; Score 50.2; DB 8; Length 5360;
Best Local Similarity 47.3%; Pred. No. 5.2; Mismatches 168; Indels 0; Gaps 0;
Matches 151; Conservative 0

QY 1744 TTCAATTTTCGATGTCGTTTGAACCTTCTTTTGTGATTCCTTCGATGTATCGCC 1803
DB 14 TTGTTTTTTTTTATTTGATATAAAGATTTTATATTTTGTATTTGTTAGCGTTTA 73

QY 1804 TGATAGATGGGTATACGTTAACCTTTTCTTACTGTTACTTTTCAGTCTGTGCTTC 1863
DB 74 TTTTAAATTTATTTGTTTTTATTTTGTGTTTTTAAATTTATAGAAATTTGTAGTTA 133

QY 1864 TACTTCTCATTTAATAGTTTAAAGTTTAAATTTTGGCTAAATCCACATTTTAACT 1923
DB 134 TTTAAATAGTTATGTTTGTGTTTAAATTTAGAAATTTATGATTTATTCGATTTGTTTCGTTT 193

QY 1924 TGAATCTTCCATGAAATTTGAGCTCAAAATATATACCATGAAATTTGTTGTTCTTA 1983
DB 194 TGAATGTTTATTTTGTGTTTAAATATTTTAAATGTTTGTGAAATTTTAAATTTT 253

QY 1984 GTTCTATTCTTCTGCTTCTTCTTCTTATTTTGTGTTAGATCCATTCCTACGAAAG 2043
DB 254 TTTTGTATTTTATGATGTTGCTGTTTTTAAATGGAATAATAAATTTTGTGTAATATG 313

QY 2044 GCAATGCTTTTGCATAATAT 2062
DB 314 TAAATTTATAGTAGTTT 332

RESULT 11
US-09-925-065A-834303
; Sequence 834303, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 834303
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-834303

Query Match 1.7%; Score 49.8; DB 6; Length 613;
Best Local Similarity 51.7%; Pred. No. 3.3;
Matches 140; Conservative 0; Mismatches 127; Indels 4; Gaps 1;

QY 1654 GAAACATACCTACTACTTCATCTCCGGCTTCTCTGCTTCTTACATCTATTACCTTAAAC 1713
DB 5 GTAATGTATCATTTTTTTCATGCTGACTTTATGTAATCAATGTCTCTATTATTTTAT 64

QY 1714 TCAACGTTTACGTCGCCAAAGGTACTTTTTTCAATTTTCGATGTTCTGTTTGAACCTT 1773
DB 65 TTTTAGTTAGTCTGCTAAAGTTTTTCTATTTGTTTATCTTTGCTTCATTGA---TA 120

QY 1774 TCTTTTGTGATTCCTTCGATTTGATCGCTGATAGATGTTGTTATACGTTAACCTTTT 1833
DB 121 TTTTGTATTTGTTTCTTTGTTTAAATTTCAATTTATTTCTGCTCTGATCTTTATTATTCG 180

QY 1834 TTTCTACTGTTTACTTTTCTGCTTCTTCTACTTCTCATTTTAATAGTTTAAAGTTTA 1893
DB 181 TTTCTCTACTAAATTTGCGTTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240

QY 1894 ATATTTTGGCTAAATCCACATTTTAAAGTT 1924
DB 241 ATAAAGTTGTTCAATGAAGTTTTTCTACTT 271

RESULT 12
US-09-925-065A-834302
; Sequence 834302, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 834302
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-834302

Query Match 1.7%; Score 49.4; DB 6; Length 613;
Best Local Similarity 51.3%; Pred. No. 4;
Matches 139; Conservative 1; Mismatches 127; Indels 4; Gaps 1;

QY 1654 GAAACATCTCTACTTCACTCCGGCTTCTCGGTCTTACATCTATTACCTTAAC 1713
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
5 GTAATGATCATATTTTCATGCTGCTGACTTTATGTAATTCAAATGCTCTATTATTTTAT 64

QY 1714 TCAACGTTTACGCCCAAGGTTACTTTTTCATTTTCGATGCTCTGTTTGAACCTT 1773
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 TTTTAGTAGTCTGGCTAAAGTTTTTCTATTTTGTGTTATCTTGTCTCATGCA----TA 120

QY 1774 TCTTTTGTGATTCCTTCGATTCATCGCTGATAGATGTTGTTATACGTTAAACCTTTT 1833
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 TTTTGTATGTTTCTTGTGTTAAATTCATTTATTTCTGCTGATCTTTATTTTGT 180

QY 1834 TCTTACTGTACTTTCAGTCTTCTGCTTCTTCTACTTCTCAATTAATGATTTTAAAGTTA 1893
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 TTTCTTCTACTAATTTTGGGTTTGTGTTCTGCTTTTCTTAATTTCTTAAATTCCTTAAAGTGCATC 240

QY 1894 ATATTTTGTGCTAATCCACATTTTAAAGTT 1924
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 ATAAAGTTGTTCAATGAAGTTTCTTACTT 271

RESULT 13
US-10-821-234-2/c
; Sequence 2, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 2
; LENGTH: 2409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-2

Query Match 1.7%; Score 49.4; DB 8; Length 2409;
Best Local Similarity 50.6%; Pred. No. 5.9;

Matches 119; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 2317 TCTCCATTTGCCGCTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTCTATC 2376
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1413 TGTTCATCTACTGGATTCACAGAGCCTTCATCATAGACTGGTATATTAAGCGGCTACATA 1354

QY 2377 AATGGTGACTTCTTTTACTTTGATGTTTTTGGGGTTTTTCAGGGCTCGCATTCCTCCCTGG 2436
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1353 AACCTCACCATATTTGGAAGATTCCTACTCCATTTGCAAGTCATGCTTTTCCACCTATTG 1294

QY 2437 ACGGATCTTCCAGGCTATACCGCAGTGATAGCGCTGTTTATAGTGGCGATTCATCTCA 2496
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1293 ATGGCTTTCTTCAGAGTCTACCTTACCATATATACCCCTTTTATCTTCTTCCATTACACAAG 1234

QY 2497 TAAACATCTGAGTCTTTTGTGTTTGGGAAGGATATGGACACAAGCATCCCATGA 2551
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1233 TGGTTTATTTAAGTCTGTACATCTTGGTTAATATCTGGACAATTTCCATTCATGA 1179

RESULT 14
US-10-240-708-47
; Sequence 47, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 47
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (67, 2620)
US-10-240-708-47

Query Match 1.7%; Score 49.4; DB 8; Length 5152;
Best Local Similarity 50.4%; Pred. No. 7.3;
Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1736 TTACTTTTTTCAATTTTCGATGTTCTGTTTGAACCTTCTTTTGTGATTCCTTCGATT 1795
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 66

QY 1796 GTATCGCTGATAGATTGTTTATACGTTTAACTTTTCTTACTGTTTACTTTCAGTTTC 1855
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 NTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 126

QY 1856 TTGCTCTTCTACTCTCATTTAATTAAGTTTTTAAAGTTTAAATATTTTGGCTAAATFCCAATT 1915
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
127 TTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGATTAAAGTTTGTAGTGAGT 186

QY 1916 TTTTAAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATCAAAATTTGAAT 1971
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
187 TATGATCGTGTATTGTAAATTTAGTTTGGGTAATAAAGTAAGATTTTGTTTTAAAT 242
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RESULT 15
US-11-147-606-3
; Sequence 3, Application US/11147606
; Publication No. US20050278795A1
; GENERAL INFORMATION:
; APPLICANT: Ntambi, James M.
; APPLICANT: Miyazaki, Makoto
; TITLE OF INVENTION: Stearoyl-CoA desaturase 4 gene
; FILE REFERENCE: 960296.00197
; CURRENT APPLICATION NUMBER: US/11/147,606
; CURRENT FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: 60/578,234
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 10166
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-147-606-3

Query Match          1.7%: Score 49.4; DB 12; Length 10166;
Best Local Similarity 49.4%; Pred. No. 8.9;
Matches 128; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

Qy      775  GAGTGAAGAATGCCCACTGGGTTTGGTTCTCTCTGTTTTGCTTGTTGTTGTTGTTCAA 834
Db      7902  GAGATGGACTTGCAAACTGGTTTTTGGTTTTTGGTTTTTGGTTTTTGGTTTTTGG 7961

Qy      835  AGTTTCAGCGCTTCTCTGTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCAACCTT 894
Db      7962  TTTTGTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTT 8021

Qy      895  TCCAAATATATATGTTACAAACAATTTGCTGCTAGTTTAAACAATGATAATGTTTGATGAT 954
Db      8022  TTTTGTGGTTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTT 8081

Qy      955  CTTTGGCAAGACTCCATTTTGGTTTTTAAGGTAAACCTTGAATCTCATAGATTGTCGATTGTT 1014
Db      8082  TTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTTGGTTTTTT 8141

Qy      1015  GGTATTTCCATTTTCAGGT 1033
Db      8142  GGTTTTTTGGTTTTTTGGT 8160

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Search completed: March 7, 2006, 09:42:29
Job time : 811 secs

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